

FIG. 1A

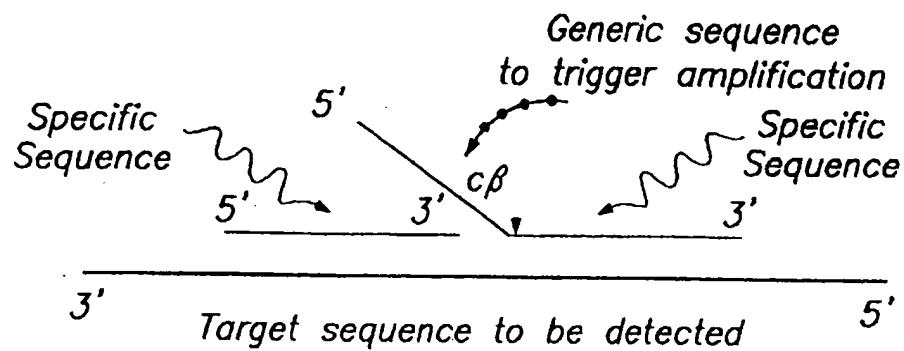


FIG. 1B PART ONE: TRIGGER REACTION

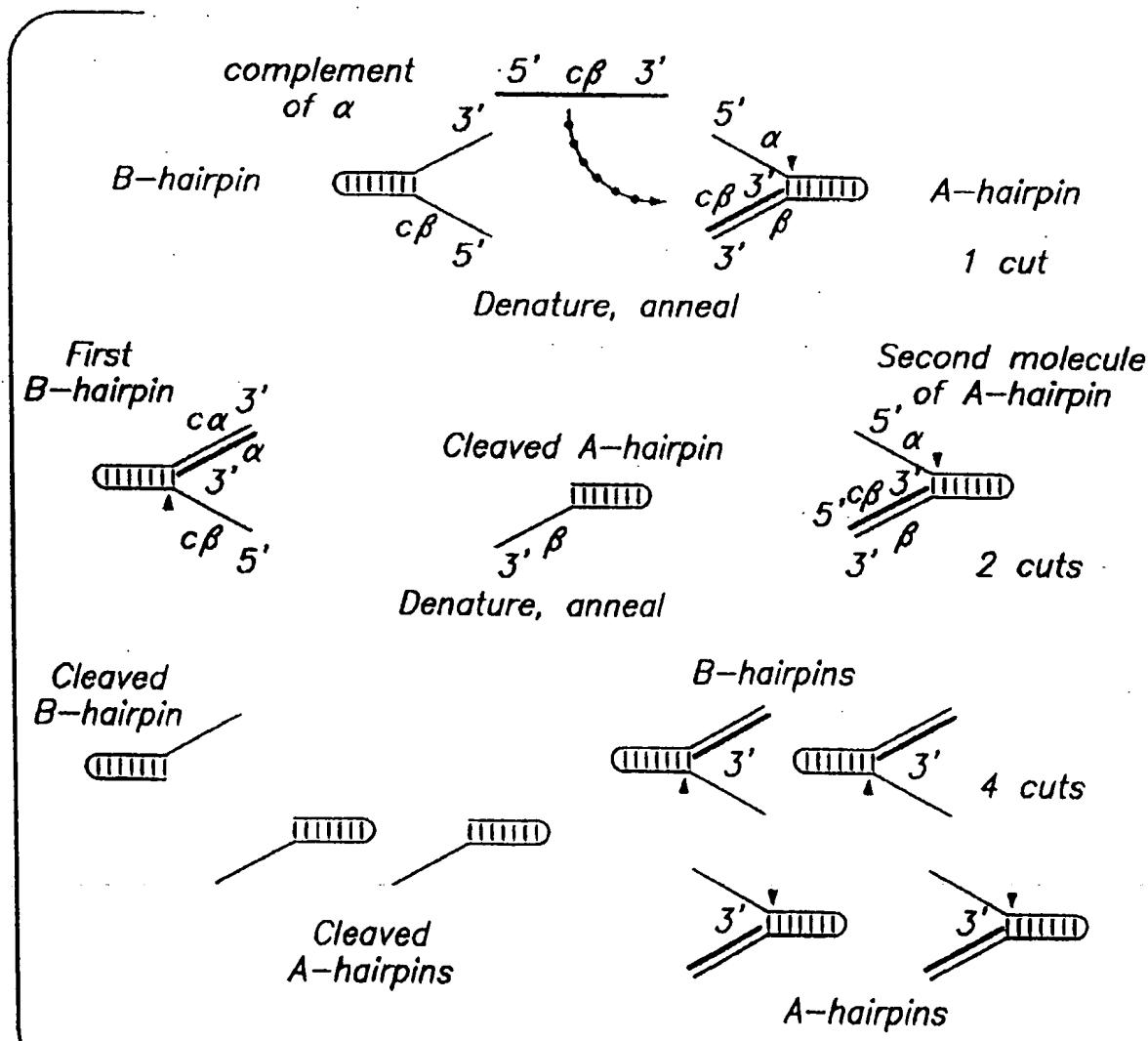


FIG. 1C PART TWO: DETECTION REACTION

FIG. 2A

FIG. 2B

FIG. 2C

MAJORITY [SEQ ID NO:7] TCCAGCCCCACATGAXGACCTGAXGCCTCTGGCAACTGCCAACCTTCCCACCGTGCACCGACCTGCCCTGGA
DNAPTAG [SEQ ID NO:1] ... T ... A ... C ... T ... A ... G ... C ... G ... A ...
DNAPTFI [SEQ ID NO:2] ... GGG ... G ... C ... GCC ... T ... C ... A ... T ... A ...
DNAPTT [SEQ ID NO:3] ... A ... C ... A ... C ... G ... T ... C ... G ... A ... T ... A ...
DNAPTTT [SEQ ID NO:4] ... C ... G ... T ... C ... G ... A ... T ... C ... G ... A ... T ...
764
765
766
767
768
769
770

MAJORITY GGTGGACTTTCGGAAAGXGGGGAAAGCCACCCGGGGCTTAAGGGCTTCTGGAGGGCTGGAGACTT
DNAPTAG ... AA ... AA ...
DNAPTFI ... GG ... G ... C ... CACA ... A ... T ... T ... GC ... T ... T ...
DNAPTT ... C ... G ...
834
835
836
837
838
839
840

MAJORITY CCCACCCCTCCACGAGTTCCGGGCTCTGGAGGGCCCAAGGGCCCTGGAGGGAGGGCCCTGGCCCCCG
DNAPTAG ... T ... AA ...
DNAPTFI ... A ... G ...
DNAPTT ... C ... G ... C ... G ... C ... G ... C ... G ... C ...
904
905
906
907
908
909

MAJORITY CGGAAAGGGCCCTGGCTGGGCTTGGCTTGGGCCCCAATCTGGGGCCGAACTCTGGCCCTGGC
DNAPTAG ... G ... AAG ... AAG ...
DNAPTFI ... T ... T ... T ... T ... T ... T ...
DNAPTT ... C ... G ... C ... G ... C ... G ... C ...
974
975
976
977
978
979

MAJORITY CGCCCCAGGGGGGCTGGCACAGACCCCTTAXGGGACCTXAAGGAGGT
DNAPTAG ... G ... G ... G ... G ...
DNAPTFI ... T ... GG ... G ... G ... G ... G ... G ...
DNAPTT ... TG ... G ... G ... G ... G ... G ... G ...
1044
1045
1046
1047
1048
1049
1050

FIG. 2D

MAJORITY [SEQ ID NO:7] CGGGGACTCTCGGGAGGACCTGGGGGTTTGGGGCTGAACGGAGGGCTXGACCTGXTGGGGGAGG
DNAPTAQ [SEQ ID NO:1] G. 1 A. AG. C. A. T. G. CC. C. 1114
DNAPTFI [SEQ ID NO:2] AA. G. G. C. G. T. C. A. A. 1111
DNAPTH [SEQ ID NO:3] C. C. C. C. T. C. C. G. G. 1120

MAJORITY ACCCCATGGCTGGCTAACCTCCCTGGACCCCTCAACACCAACCCCCAGGGGGCTGGGGGGCTACCCACGG
DNAPTAQ T 1184
DNAPTFI G T 1181
DNAPTH G 1190

MAJORITY CGGGGAGTGACGGAGGAXGGGGAGGGGGCTGGTXXCTGGGAGAAGGGCTCT1CCXGACCTXXXGGAG
DNAPTAQ C. G. G. T A. A. CCC. CCC. GTG. G. 1254
DNAPTFI C. CCC. C. C. C. C. A. C. AAA. 1251
DNAPTH C. CCC. C. G. C. G. CAT. G. CCTTA. 1260

MAJORITY CGGCTTGGGGGGAGGAGGGCTGGCTTACCGGAGGTGGAGAAGGGCTTTCCGGGGTCTGG
DNAPTAQ A. G. 1324
DNAPTFI A. A. A. AC. C. G. G. G. G. G. 1321
DNAPTH C. A. C. C. C. A. C. C. C. C. 1330

MAJORITY CCCACATGGAGGGCACGGGGCTXGGGGCTGGACGTGGGGCTACCCAGGGCCTXTCCTGGGGTGGCGGA
DNAPTAQ G. 1394
DNAPTFI G. 1391
DNAPTH G. A. T. 1400

FIG. 2E

MAJORITY [SEQ ID NO:71]	CCAGATCCGGCCCTCGAGGAGGTTCGGCCACGGCTTCAACCTCAACTCCCCGGAC		
DNAPTAQ	[SEQ ID NO:11] GC GC	1464	
DNAPFL	[SEQ ID NO:2] G AG	1461	
DNAPTH	[SEQ ID NO:3] T G	1470	
MAJORITY	CAGCTGGAAAGGCTGCCTTGACGACCTTGCGGCTTCGGCAAGAACGGAGACGXGCCAAGC		
DNAPTAQ C A C	1534	
DNAPFL GC G A	1531	
DNAPTH TA T G	1540	
MAJORITY	GCTCCACCAACGGCCCTGCAGGCCCACCCATCTGGAGAAGATCCTGGAGATCTGGAGATA		
DNAPTAQ C C C	1604	
DNAPFL T G A	1601	
DNAPTH G A G	1610	
MAJORITY	CCGGGAGCTCAGGAAGCTAAAGAACGCTACATXGACCCCCCTGCCXGCCCTGGCACCCAGGACGGGCC		
DNAPTAQ G T G A	1674	
DNAPFL A C C	1671	
DNAPTH G G AAG	1680	
MAJORITY	GGCCTCCACACCCCTTCAACGAGACGGCCACGGCCACGGCTTAGTACCTCCGACCCAACCTGC		
DNAPTAQ A T C	1744	
DNAPFL G TCC	1741	
DNAPTH C G	1750	

FIG. 2

FIG. 2G

DNAPTAQ [ESD ID NO:1] 2164

DNAP/FL [S50 (0 NO:2] A..... G..... C..... C..... C..... C..... T..... 2161

UNAPITH LISTU LU MU;31 A. 270

MAJORITY CCCCTCCCCCCCCCTACCTCAACGGGGGTGAGAACGTCGGGGGG

UNAPTAQ C.....C.....A.....AG.G.....C.....C. 2234

2231
DRAFT

THE BIBLICAL MESSIAH

DONAPTAQ 1 2304

DRAFT
CG...T 2301

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MAP 10 A. 66. 2374

237
BRIEF REPORT

244
MAPPA
MATERIALE

MAP III C. C. C. A. G. AA. C. C. 2450

FIG. 2H

MAJORITY [SEQ ID NO:7] CCCCTGGAGGTGGACCTGGCCATGGGGAAAGGACTGGCTCTGGCCCAAGGAGTAG

DNAPTA0	[SEQ ID NO:1]	A.....	A.....	GA 2499
DNAPTF1	[SEQ ID NO:2]	CC.....	CC.....	.. 2496
DNAPTFH	[SEQ ID NO:3] GT .. 2505

FIG. 3A

MAJORITY	CSEQ ID NO: 83	MKAMPLIFEPKGIVLVDGHAYRPPAKLLISQEFUWVQIARCLLRLS	69
TAQ PRO	CSEQ ID NO: 43	RGH.....H.....	68
TFL PRO	CSEQ ID NO: 53	YK.....F.....	70
TTR PRO	CSEQ ID NO: 63	F.....	
MAJORITY	APSFRHEAYKAGRAPHEDPROLALIKELVDLIGLXRLEVPGYEADDVVLATLAKKAEEKSYEVILL	S.....A.....A.....	139
TAQ PRO		GG.....V.....F.....	138
TFL PRO		FI.....	140
TTR PRO			
MAJORITY	TADRDLYQLLSDRIAVLHPEGYLIPIAWLWEKYGLRPEOWDYRALXGDPSONLPGNKGIGEKTAXKLIX	D.....A.....T.....E.....	209
TAQ PRO		H.....Y.....	208
TFL PRO		A.....I.....	
TTR PRO		V.....F.....	
MAJORITY	EWGSLENLILKNLBRVKP. XXREKIXAHME DLXLSXXISXVRTOLPLEWDFAXRREPREGRAFLERLEF	K.....R.....	278
TAQ PRO		AI.....L.....D.....K.....WD.....AK.....	277
TFL PRO		IQ.....SL.....AQ.....A.....RK.....Q.....H.....	280
TTR PRO		ENV.....K.....L.....R.....LE.....R.....	
MAJORITY	GSLLHEFFGLIEXPKALEEAPWPPPEGAFVGFWLSRPEPWAELLALAARRXGRVHRAXDPLXGLRDLKEV	S.....G.....PE.....YKA.....A.....	348
TAQ PRO		R.....D.....G.....W.....L.....Q.....R.....	
TFL PRO		I.....SF.....A.....	
TTR PRO		K.....C.....D.....A.....A.....K.....	

38
FIG.
II

MAJESTY [REDACTED] NO: 83 RGLAKDOLWLAIREGLDLXPGGDPMLAYLIDPSNTIPEGVARRGEWEIAGEBALSEHLXKX

IAO PRO	[SE0 ID N0:4]	S.	G. P.	E.	A.	A.	WG 418
ffl PRO	[SE0 ID N0:5]	I.	F. E.	A.	A.	Q1	KE 417
ffl PRO	[SE0 ID N0:6]	S.	V.	AH.	HR.	LK	420
ffl PRO	[SE0 ID N0:7]	S.					

MAJORITY RLEGUEERLLWLYXEUNEKPLSRVLAHMEATGURLDVAYLQALSLEVAAE/ RALEEEVHLAHPFMNNSH

IAO PRO	R.	R.	A.	A.	A.	A.	488
TFL PRO	K.	K.	R.	R.	R.	R.	487
TTN PRO	H.	H.	L.	L.	L.	L.	490

MAJORITY OLERVILEDEGLPAIGKTEKTGHKRSTSAAVLEALREAHPIWEKILOYRELTKLKNTYIDPLPXLVHPTRG

TAC PRO	S.	D.	I.	558
TFL PRO	DR.	H.	A.	557
TH PRO	G.	L.	V.	560

21 UT PENSATORIAT CRISSSSNPNI 001 PVRIPPLGORI BSAFVAEEGXW 1VALDYSO! EIRVVL AHL SGDENL

628
627
630

卷之三

TIAQ PRO	E.	R.	698
TITFL PRO	S.	G.	697
			700

FIG. 3C

MAJORITY [SEQ ID NO: 8] SFPKURAWI EKTLFGRRAGYVETLFGARRYVPOLNARWKSVERAERHAFNMPVQCTAADLHKLLAMVKL

768

767

770

E

TAQ PRO

[SEQ ID NO: 4]

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Genes for Wild-Type and Pol(-)DNAPtaq

Domain Coding Regions: 5' Nuclease
FIG. 4A (wt)

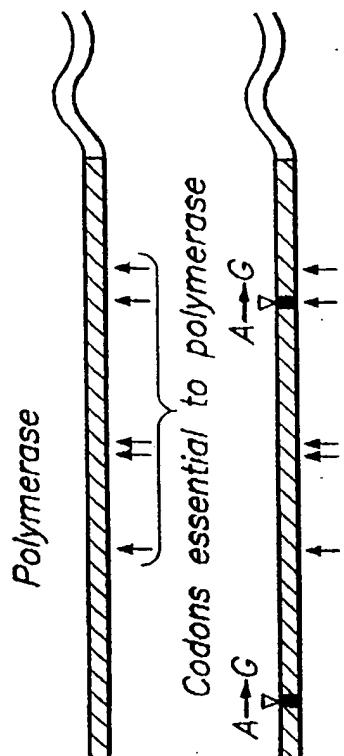


FIG. 4B



FIG. 4C

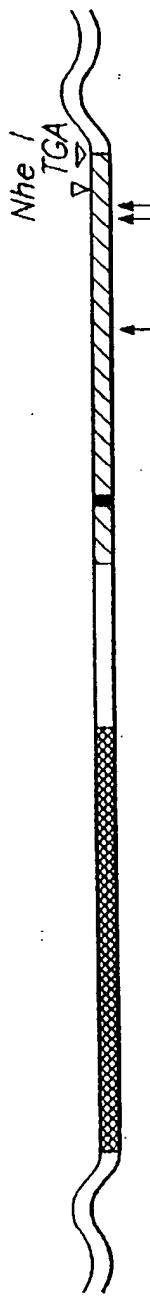


FIG. 4D



FIG. 4E



FIG. 4F

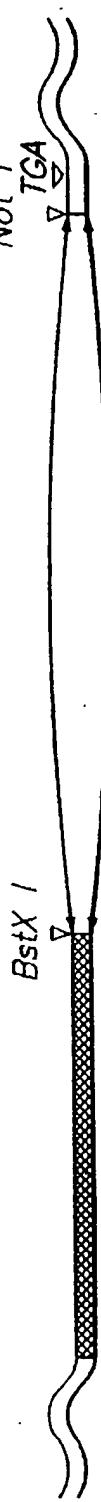
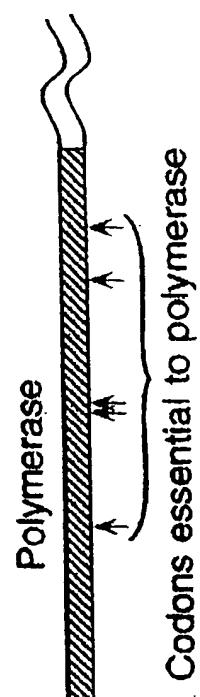
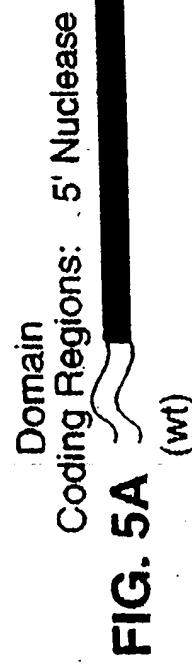


FIG. 4G

Genes for Wild-Type and Pol(-) DNAPT^{II}



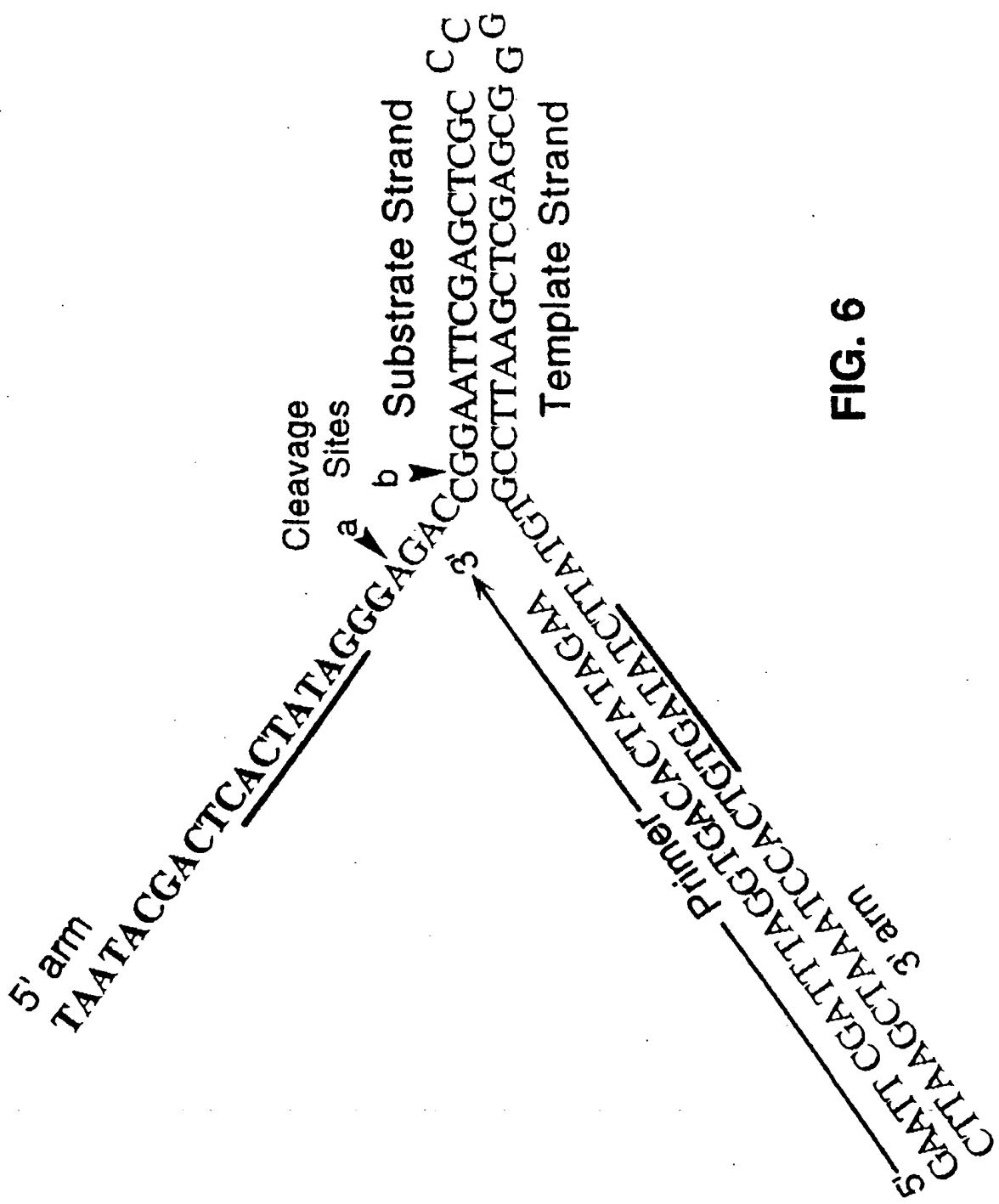


FIG. 6

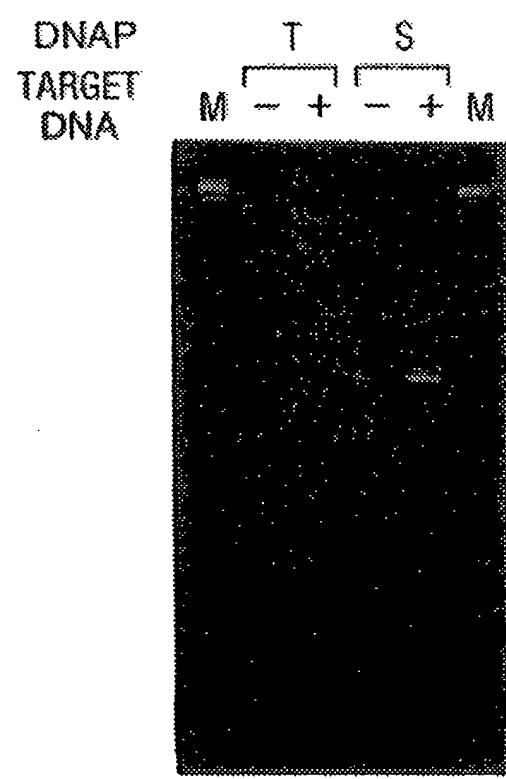


FIG. 7

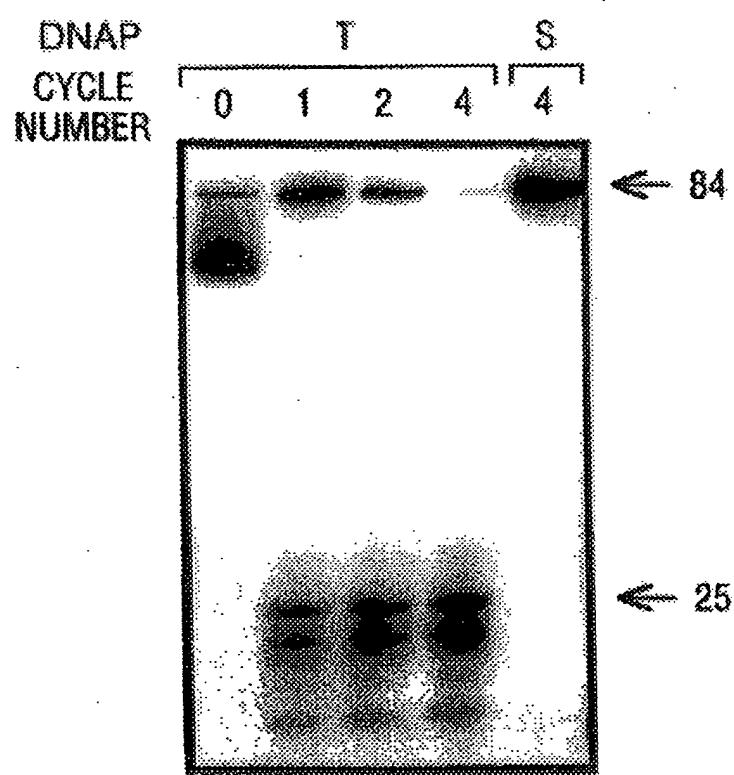


FIG. 8

	1	2	3	4	5	6
DNAP-T:	-	+	+	+	+	+
MgCl ₂ :	+	-	+	+	-	+
dNTPs:	+	-	+	-	+	-
Primers:	+	-	+	+	-	-

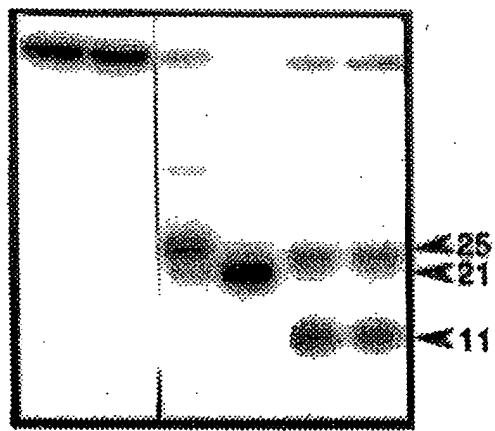


FIG. 9A

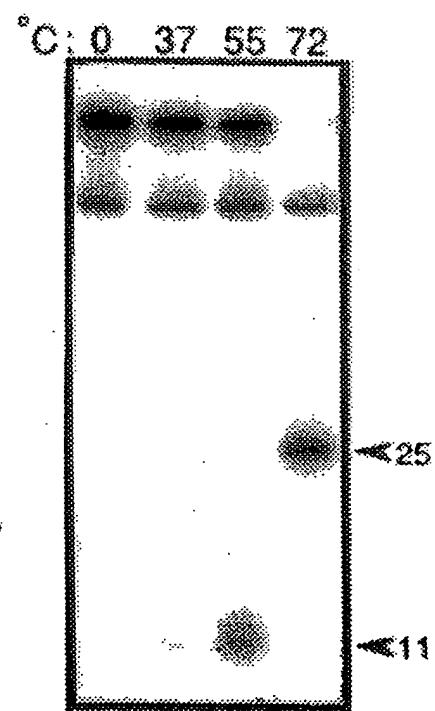


FIG. 9B

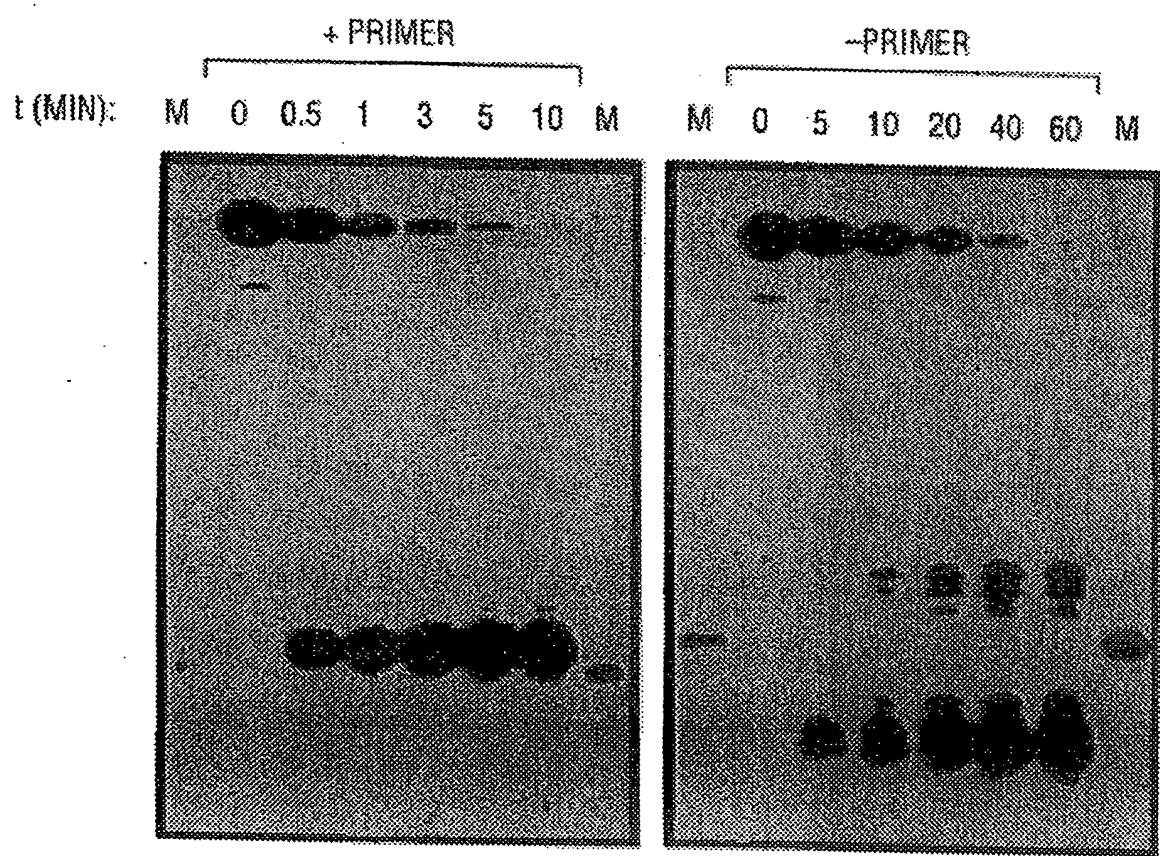


FIG. 10A

FIG. 10B

DNAP: - *Pfu* *Tag* *Tth* *Tth* *Tth* - - *Tag* *Eco* *Kin*

Primer: - + + - + - + + - + + - + +

Uncut >

25 >
21 >

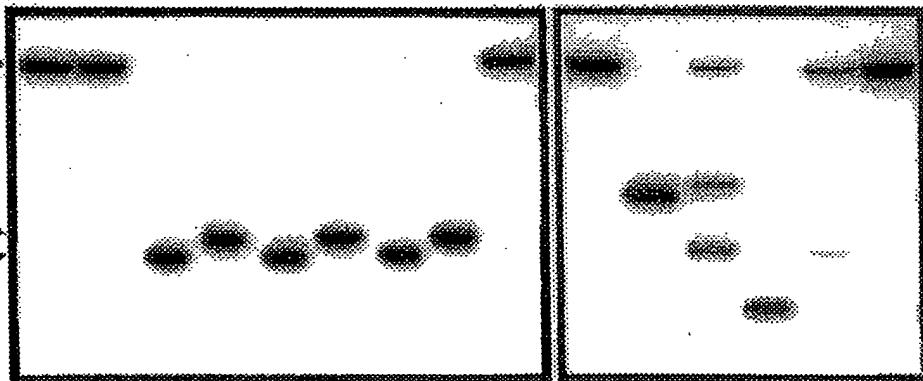
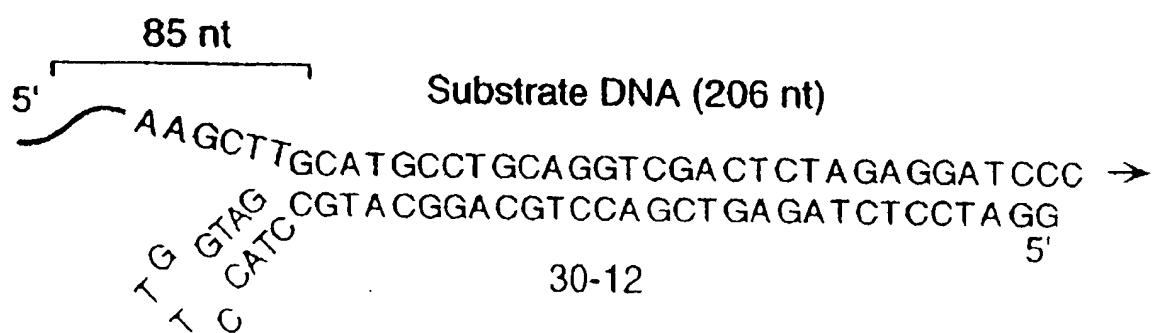
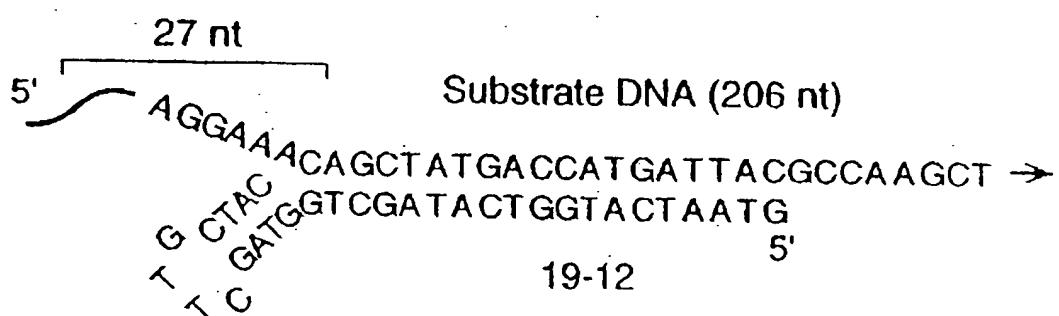


FIG. 11A

FIG. 11B

<21
<11
<<dNMPs>

FIG. 12A



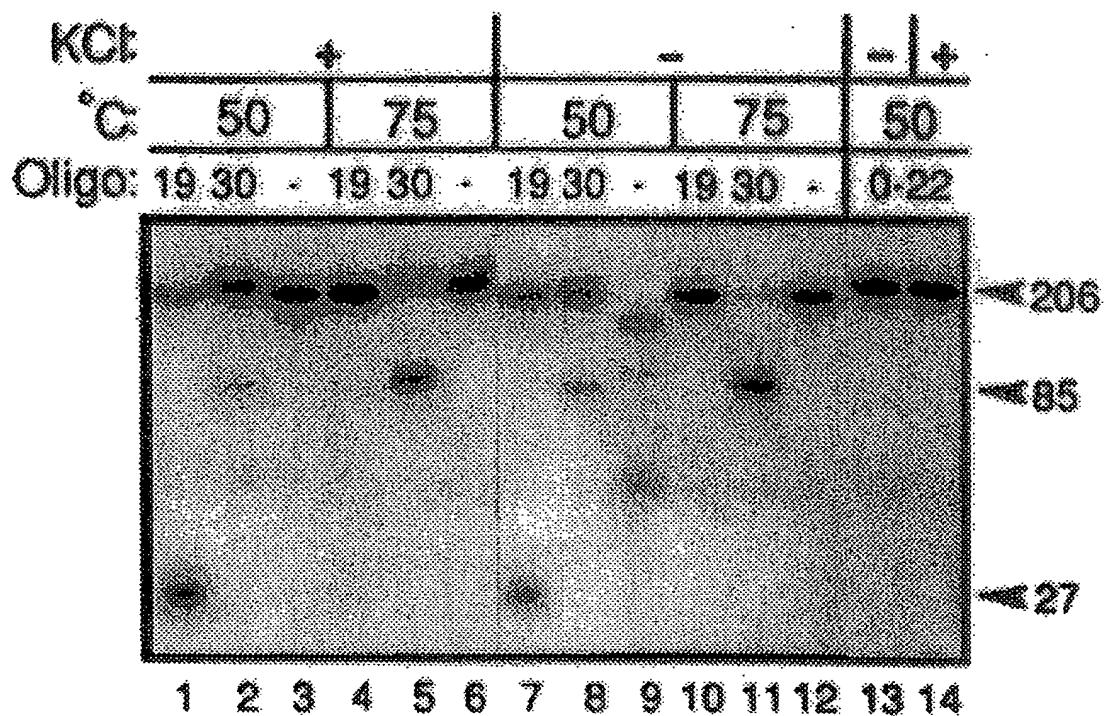


FIG. 12B

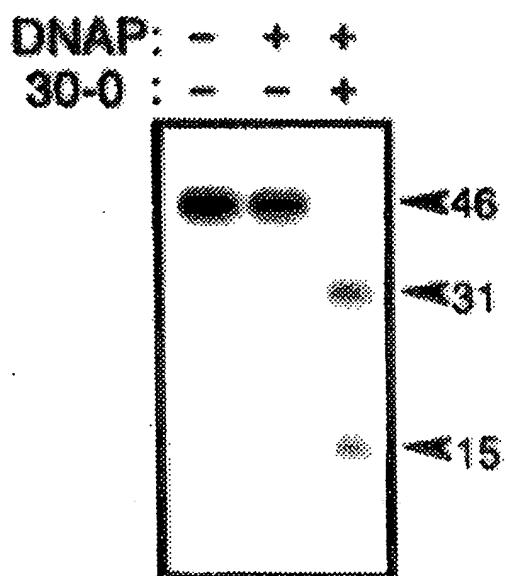


FIG. 13B

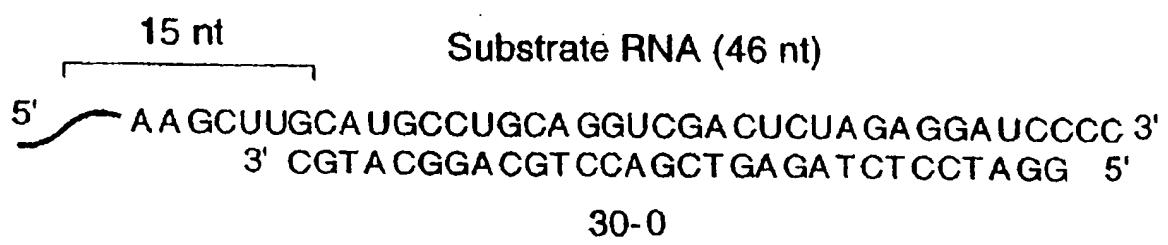


FIG. 13A

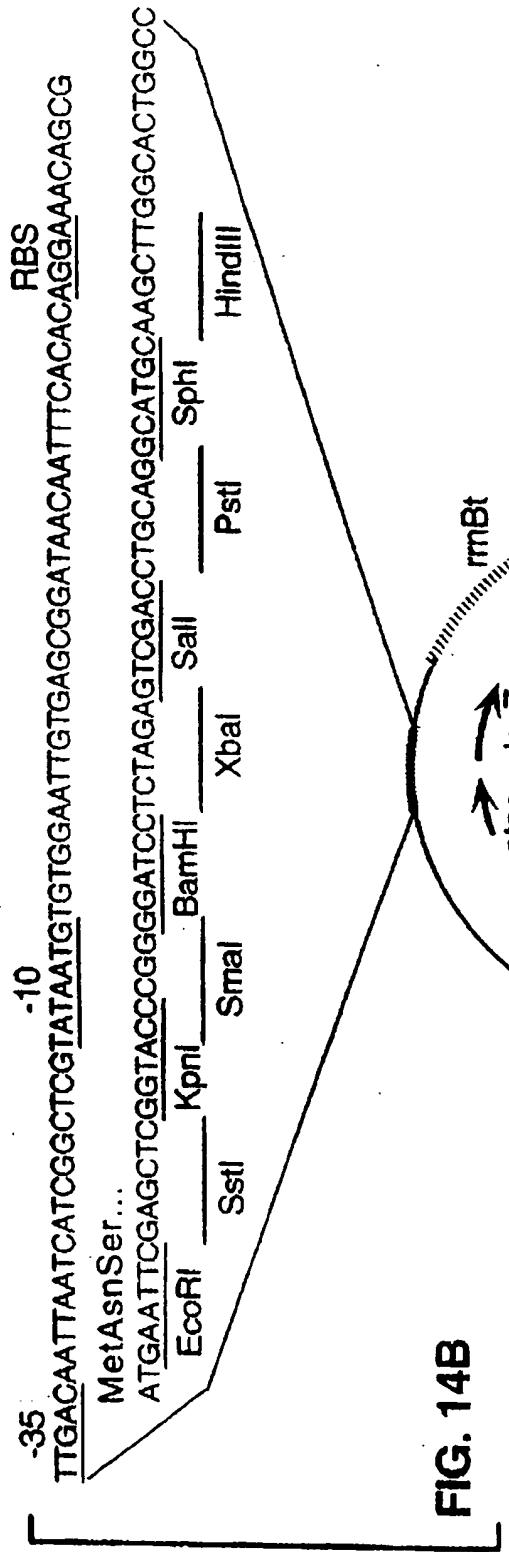


FIG. 14B

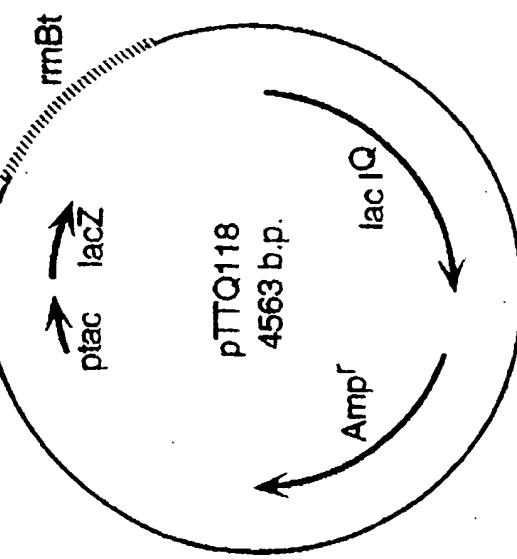


FIG. 14A

RBS: Ribosome binding site
 lacZ: Beta-galactosidase alpha fragment
 ptac: Synthetic tac promoter
 rmBt: E. coli rmB transcription terminator
 lacIQ: Lac repressor gene

FIG. 14C

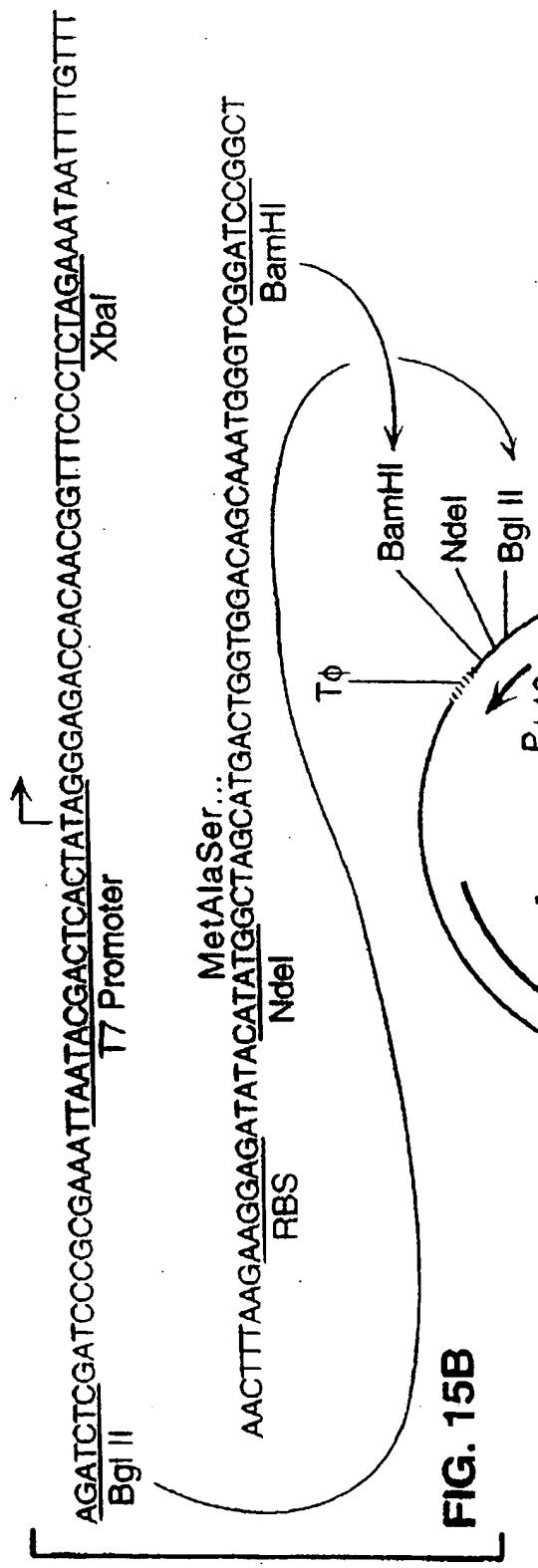


FIG. 15B

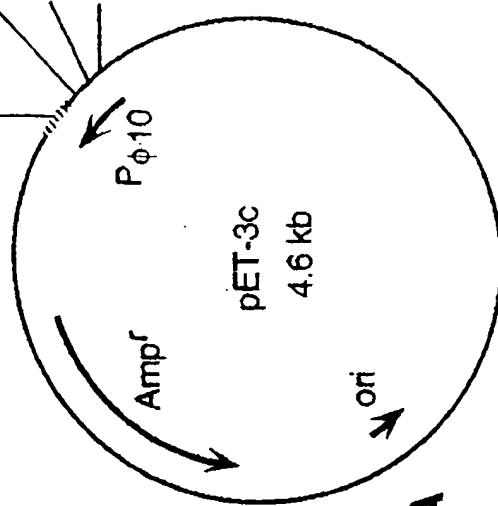


FIG. 15A

RBS: Ribosome binding site

P ϕ 10: Bacteriophage T7 ϕ 10 promoter

TΦ: T7 Φ Terminator

FIG. 15C

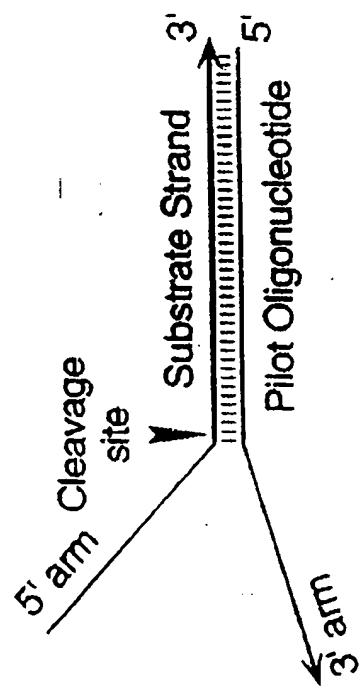


FIG. 16A

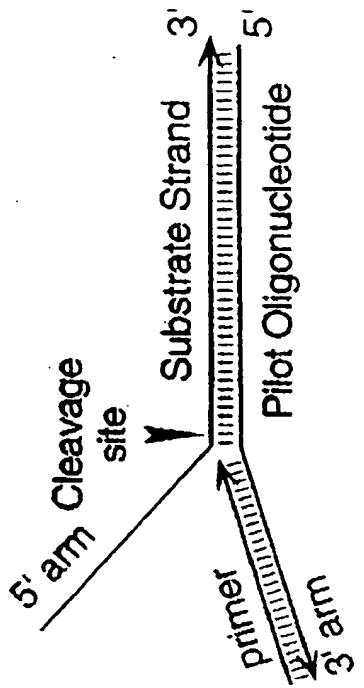


FIG. 16B

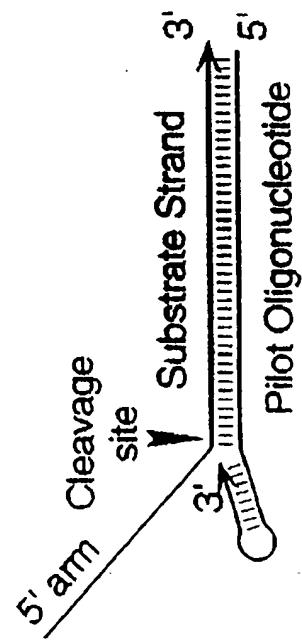


FIG. 16C

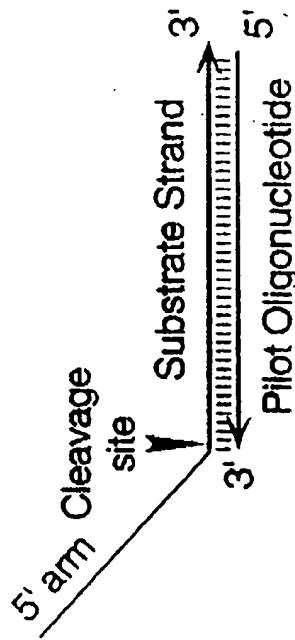


FIG. 16D

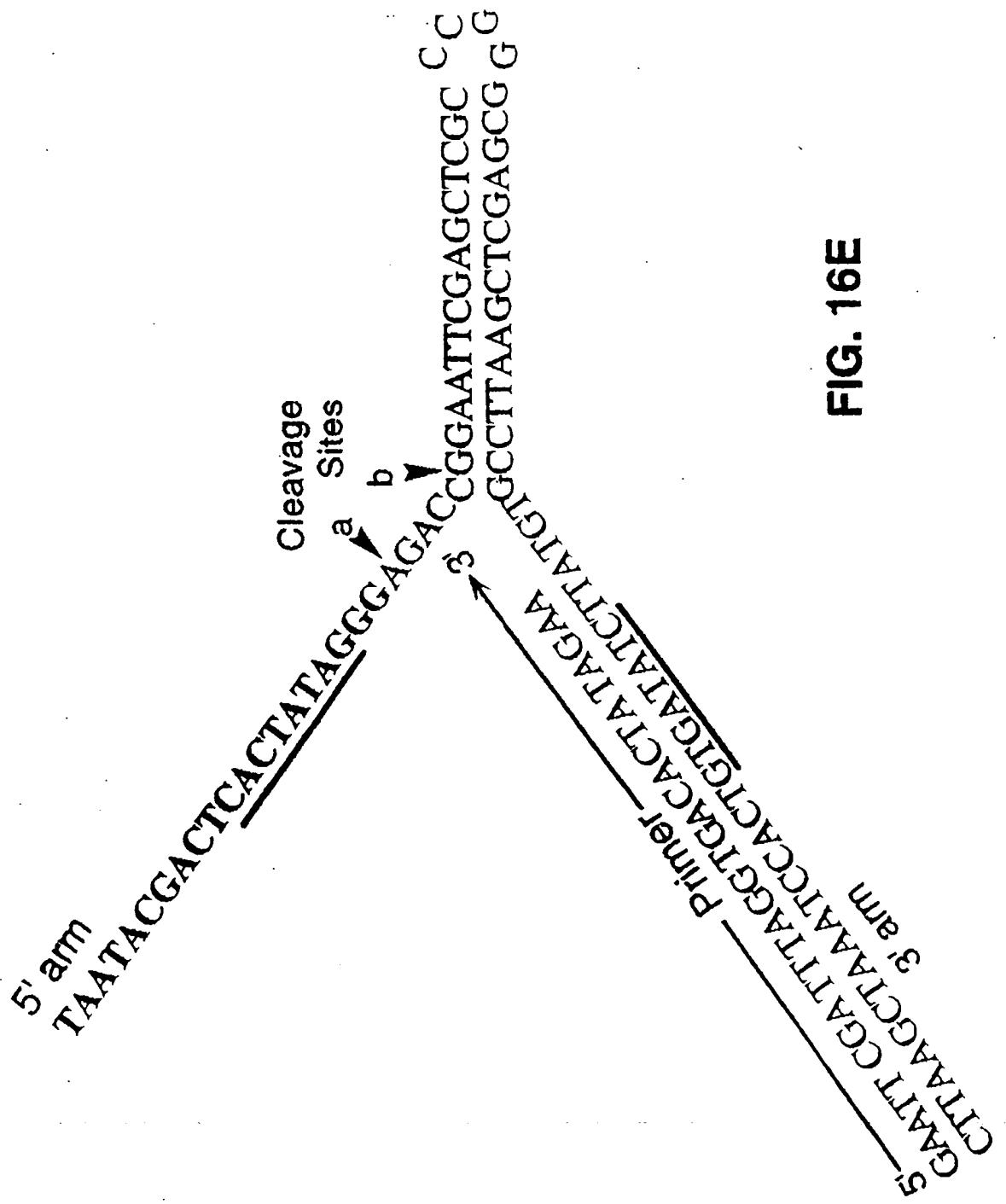


FIG. 16E

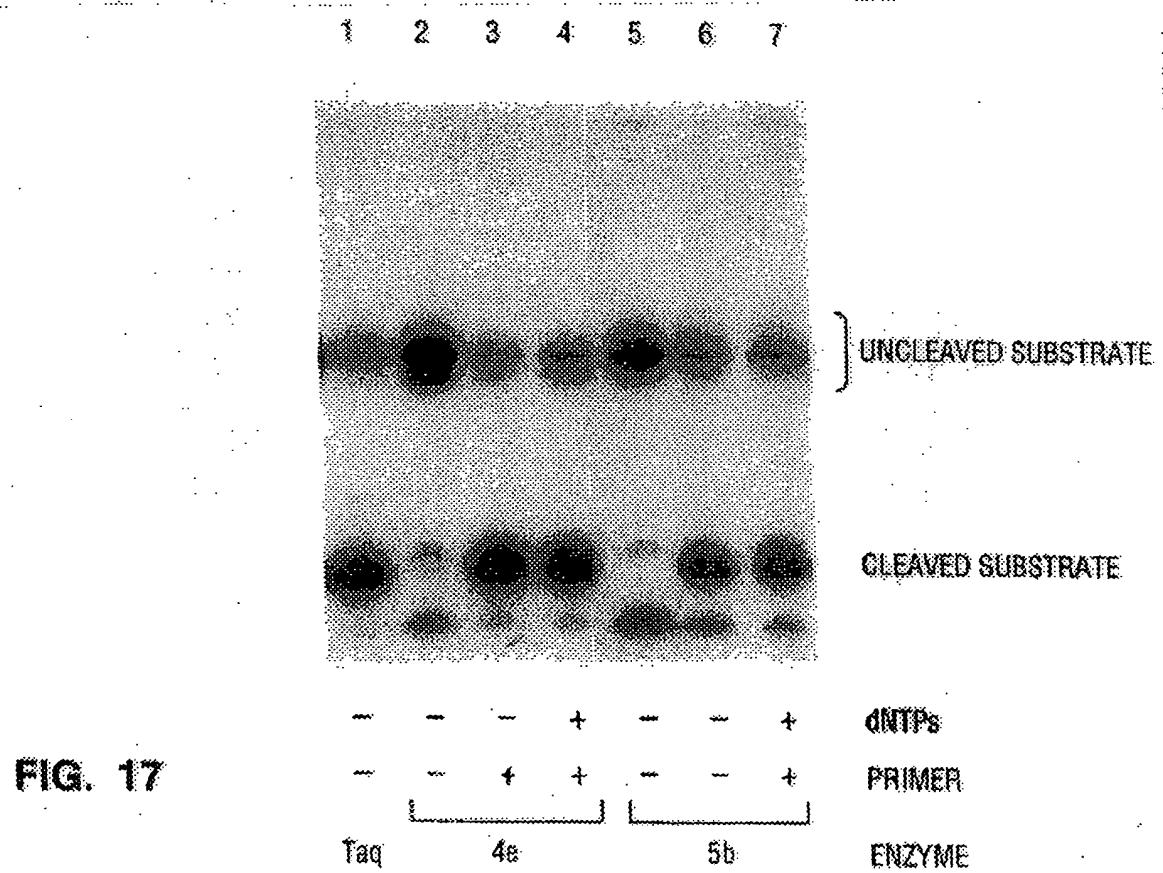


FIG. 17

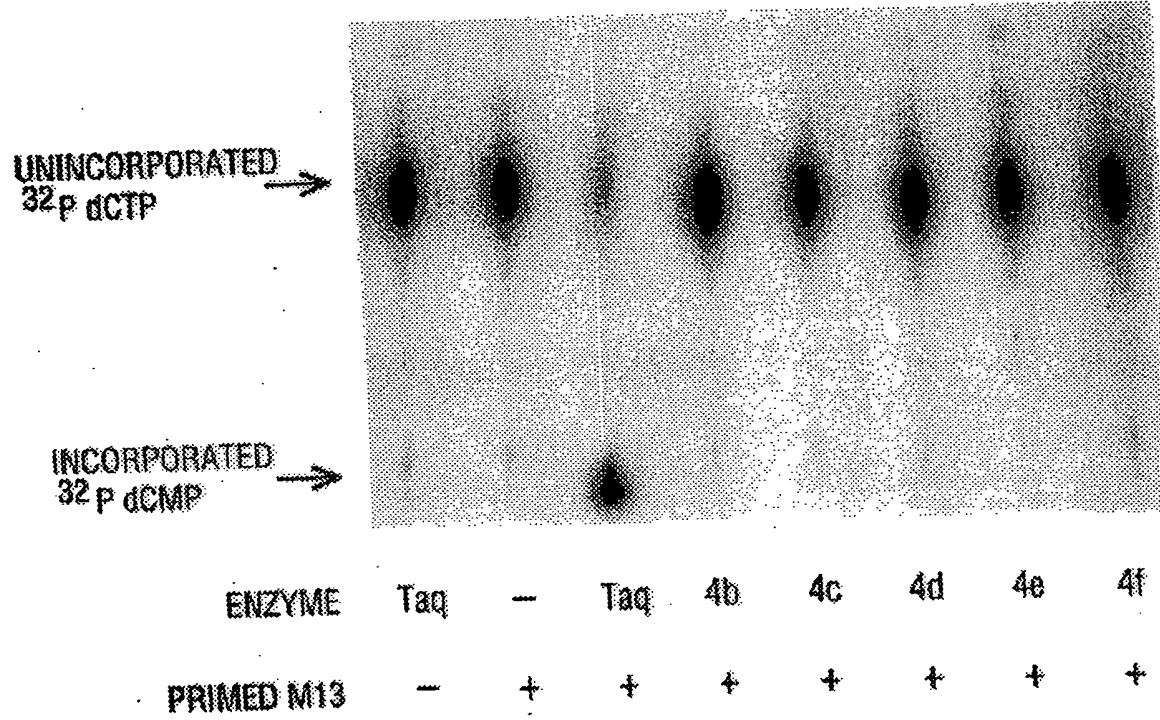


FIG. 18

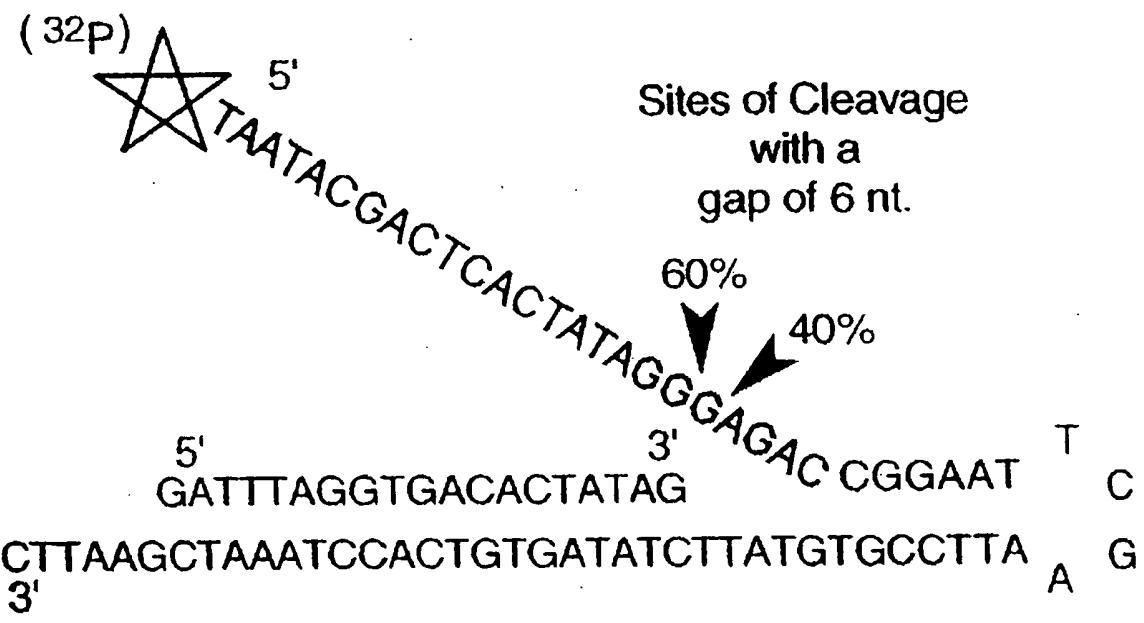


FIG. 19A

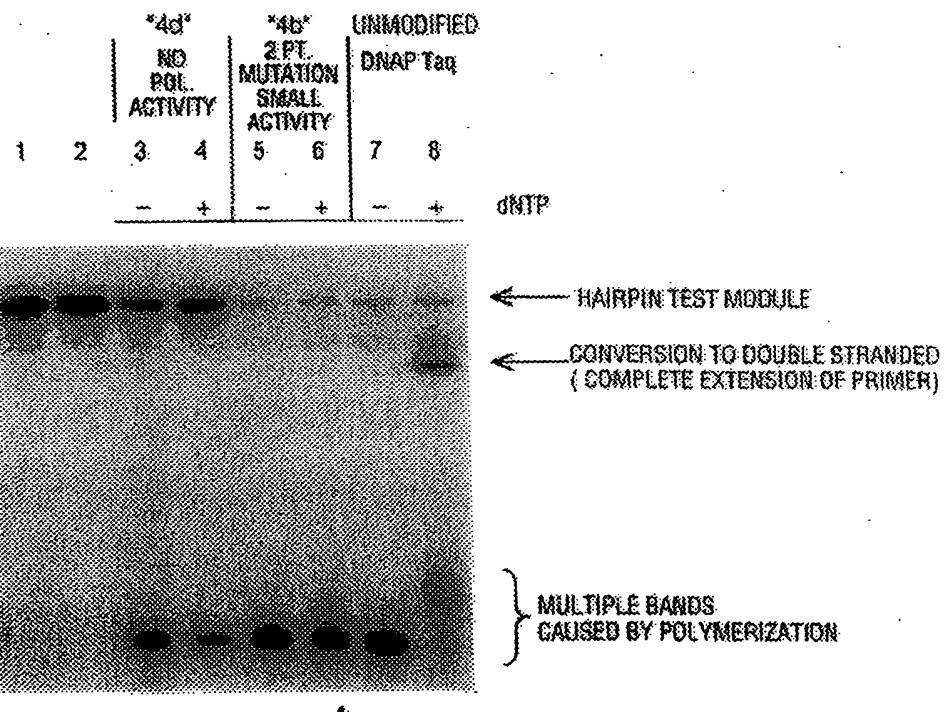


FIG. 19B

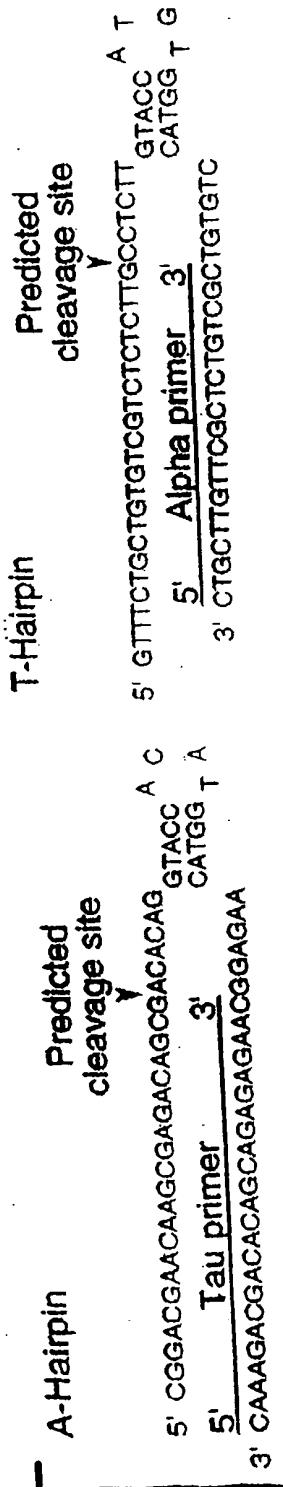


FIG. 20A

Sequence of alpha primer:
 5' GACGAACAAGCGAGACAGCG 3'

FIG. 20B

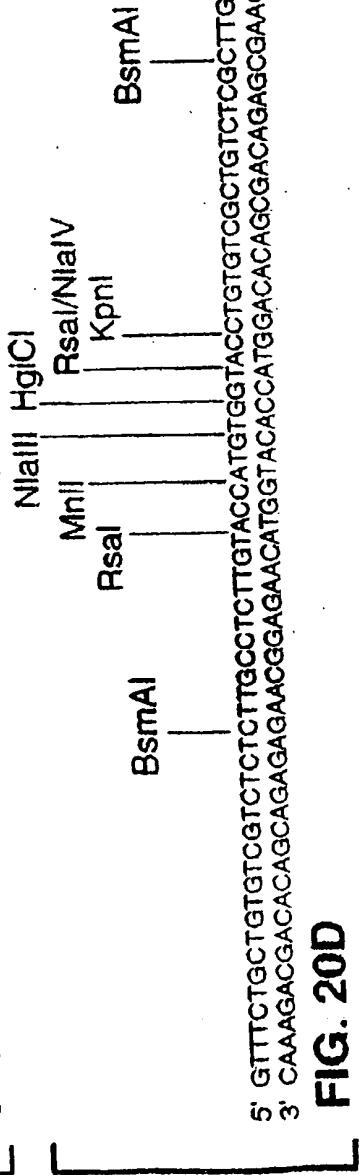
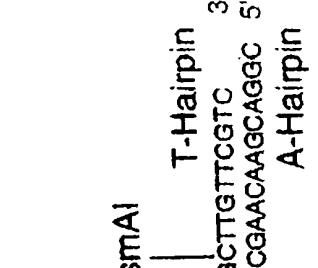
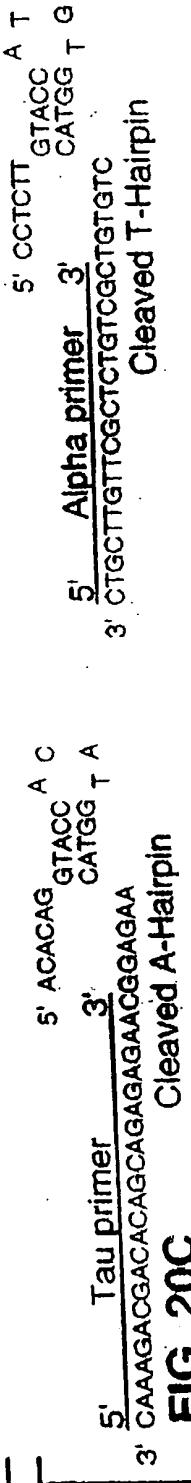


FIG. 20D

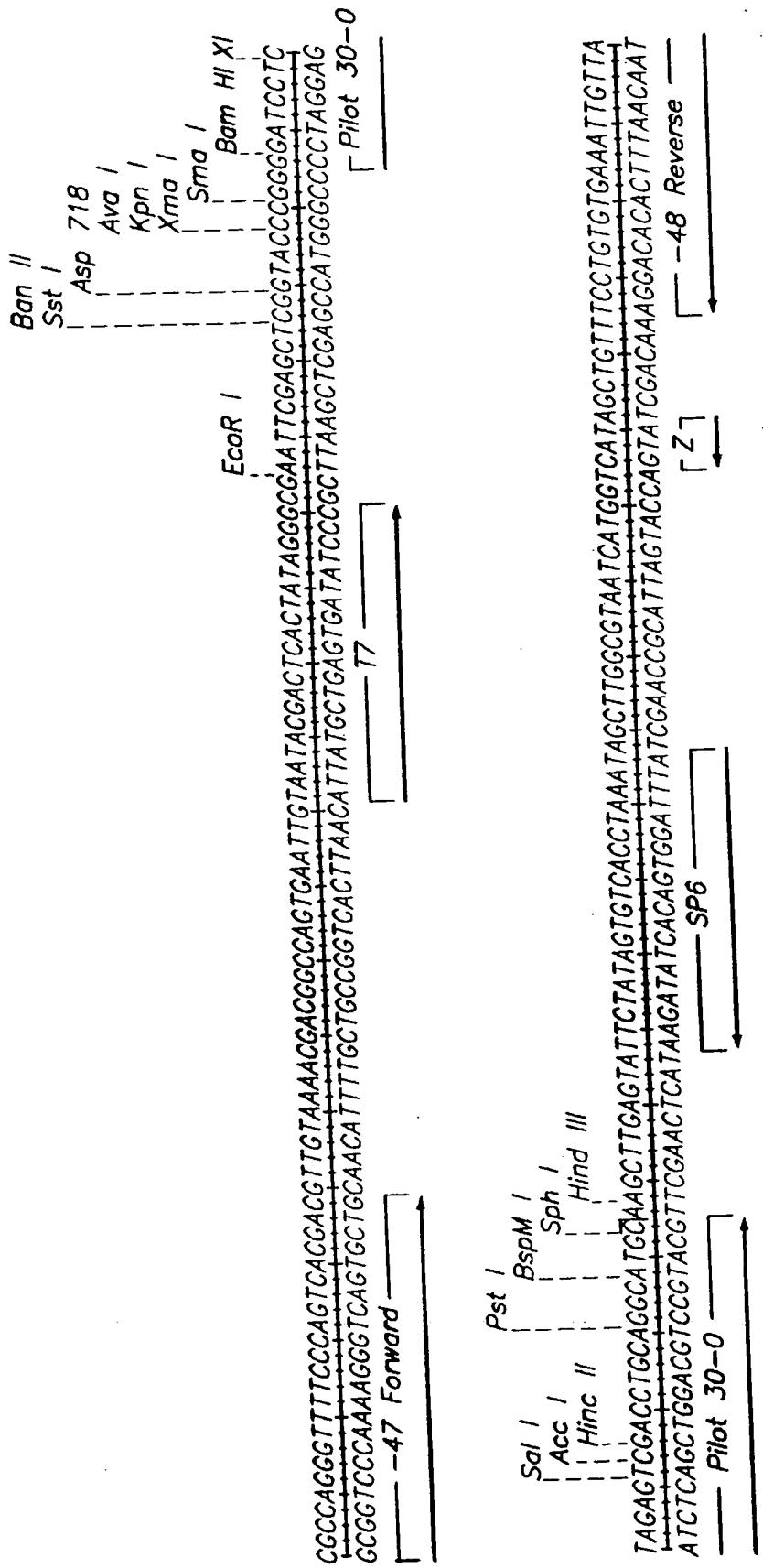


FIG. 21

TCCGCTCACAAATTCCACACAACATACGA 228
 AGGGGAGGTAAAGGTGTGTTGATGCT
 -48 Reverse
 — 206

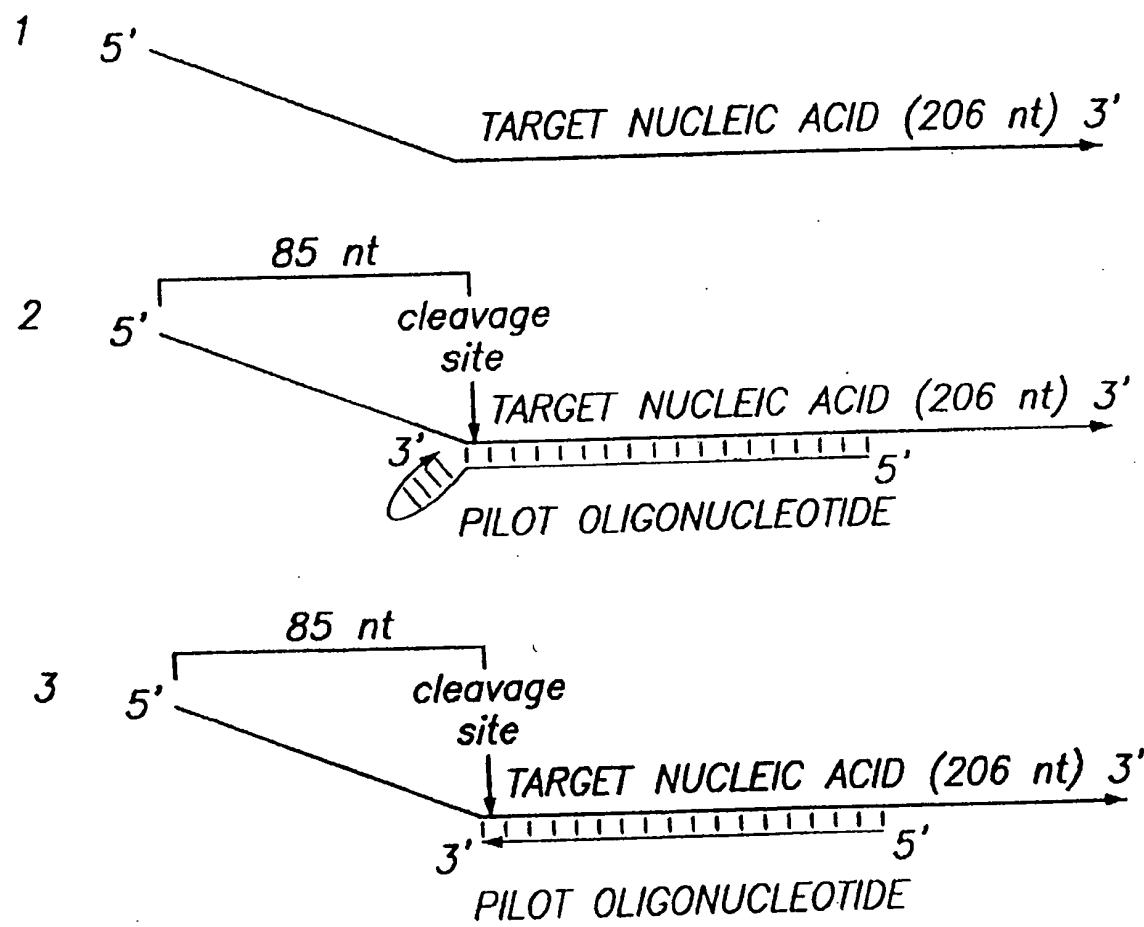


FIG. 22A

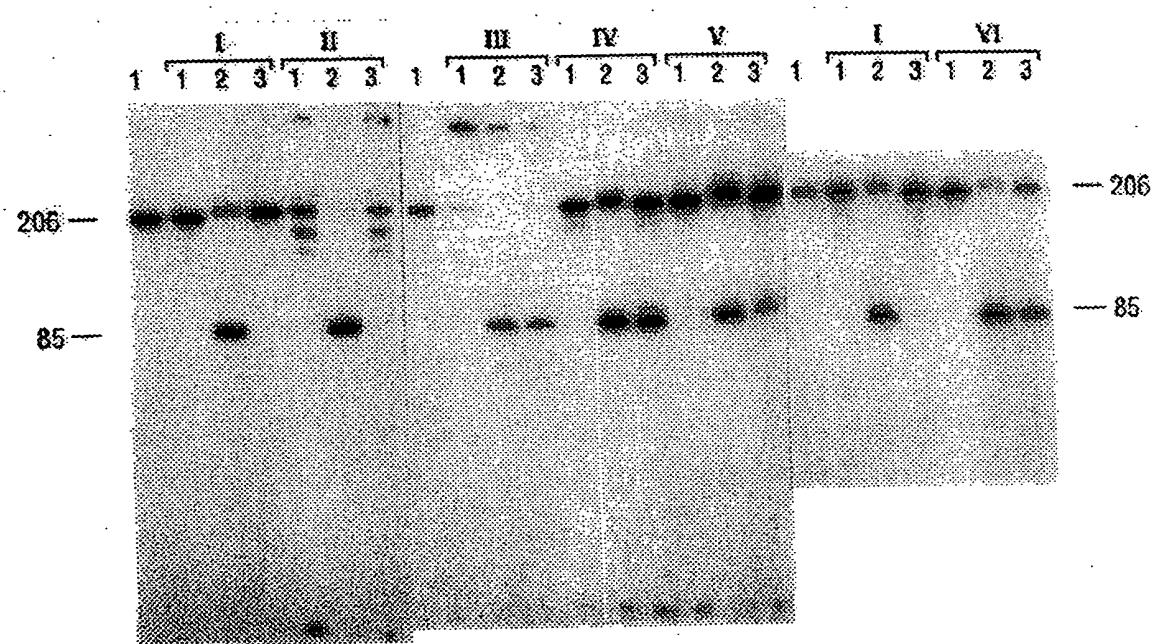


FIG. 22B

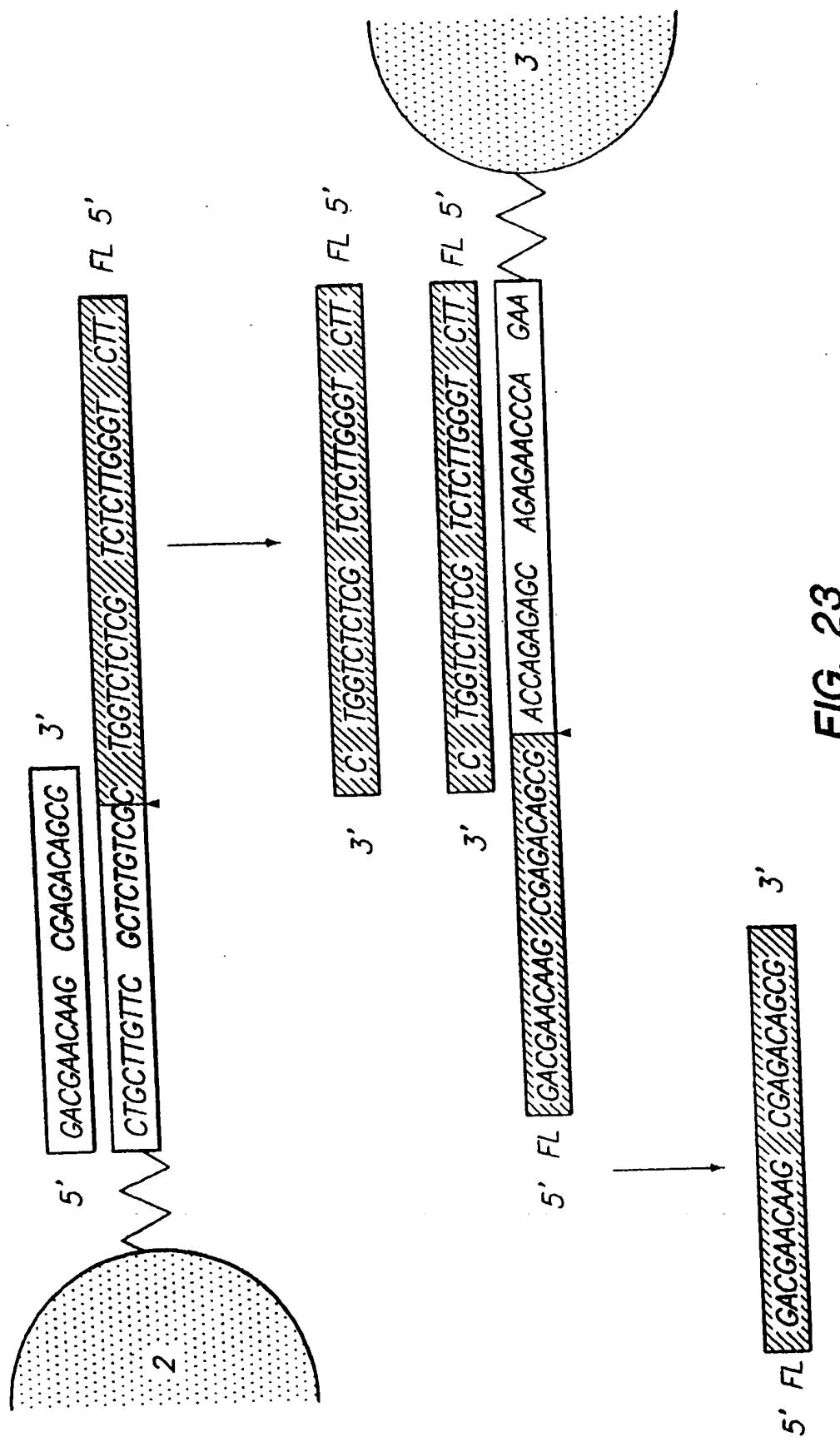


FIG. 23

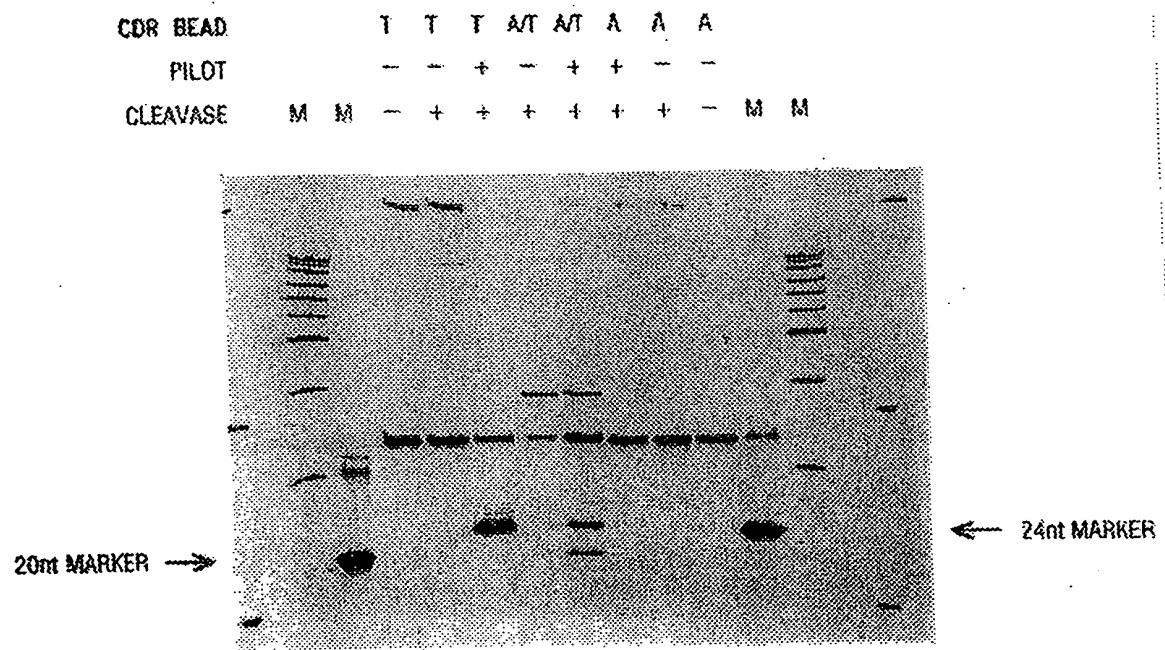


FIG. 24

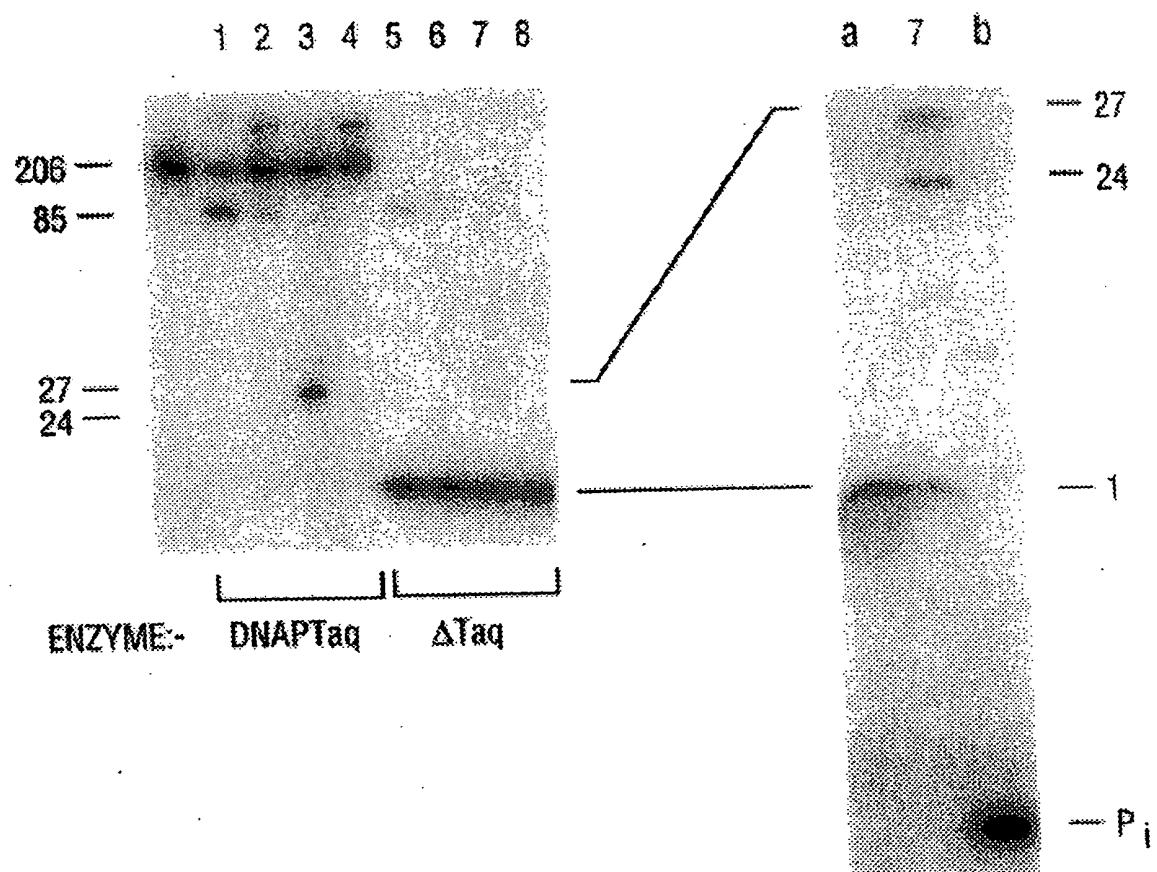


FIG. 25A

FIG. 25B

FIG. 26A

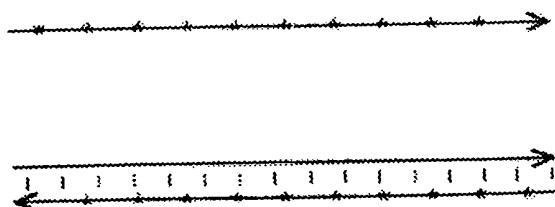
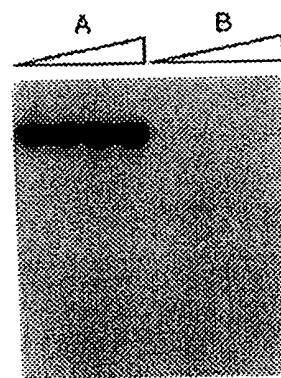


FIG. 26B

$\star \approx 32P$



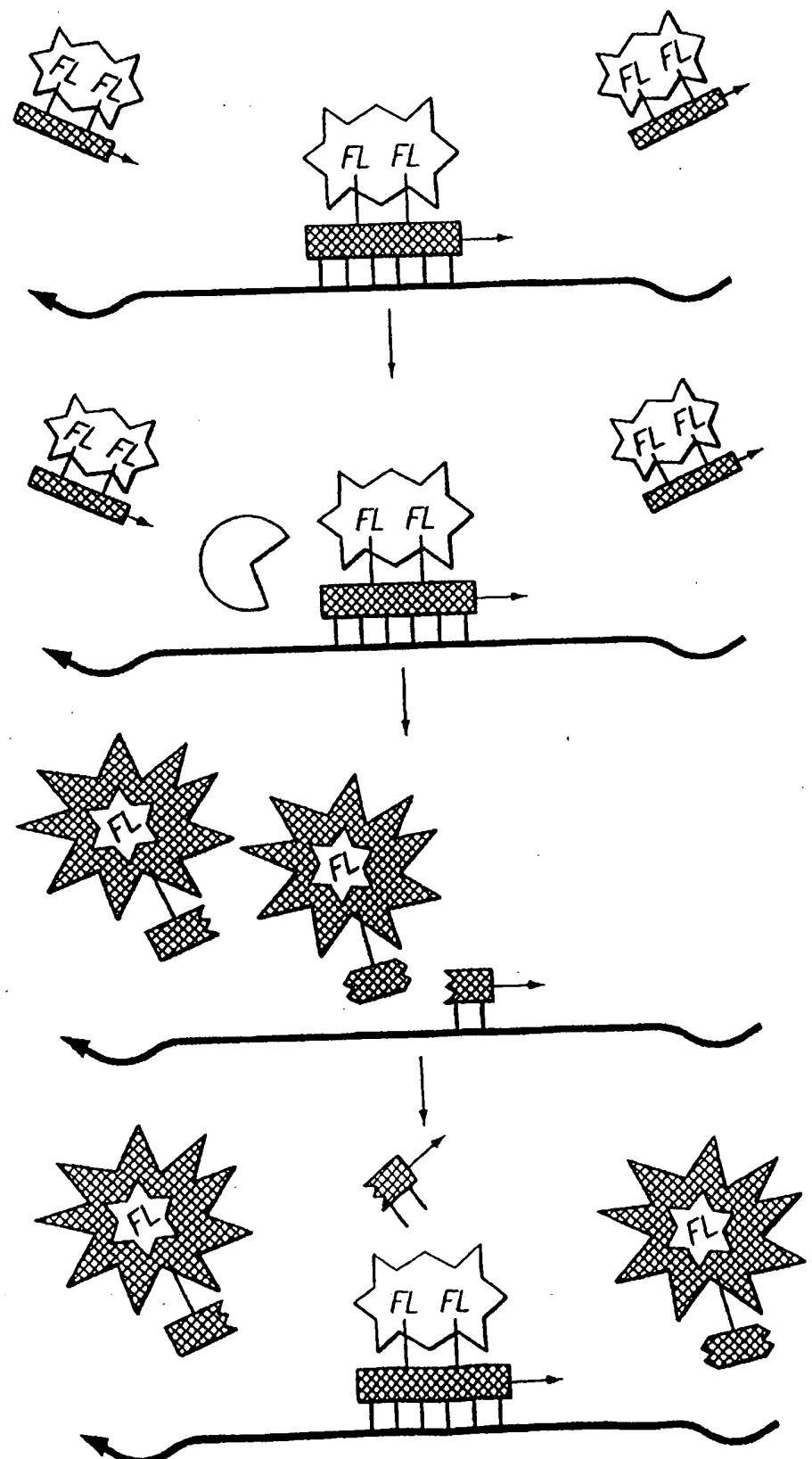


FIG. 27

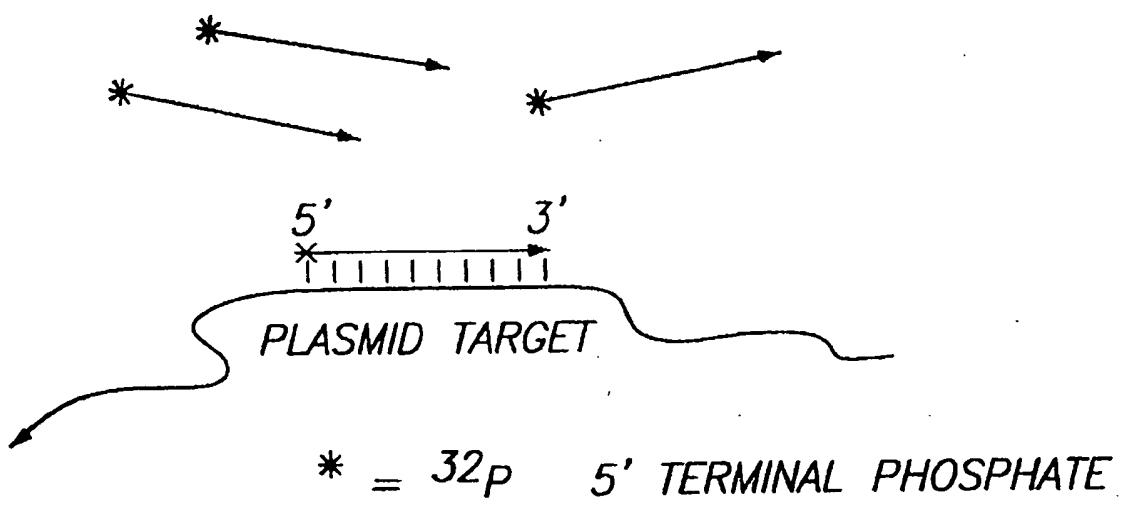


FIG. 28A

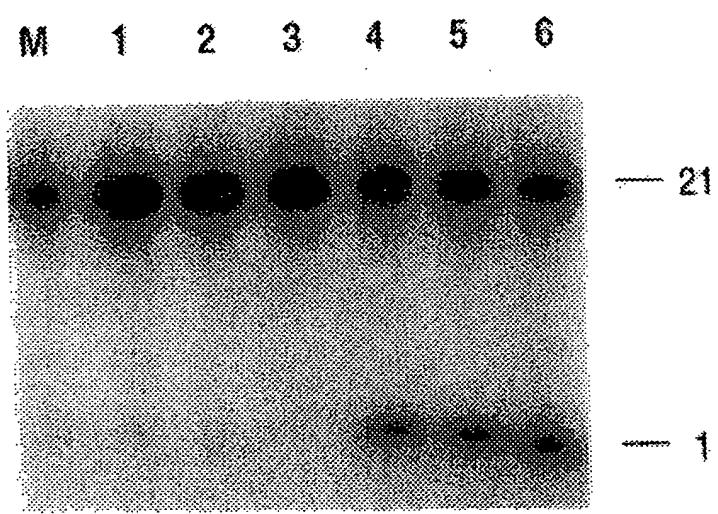


FIG. 28B

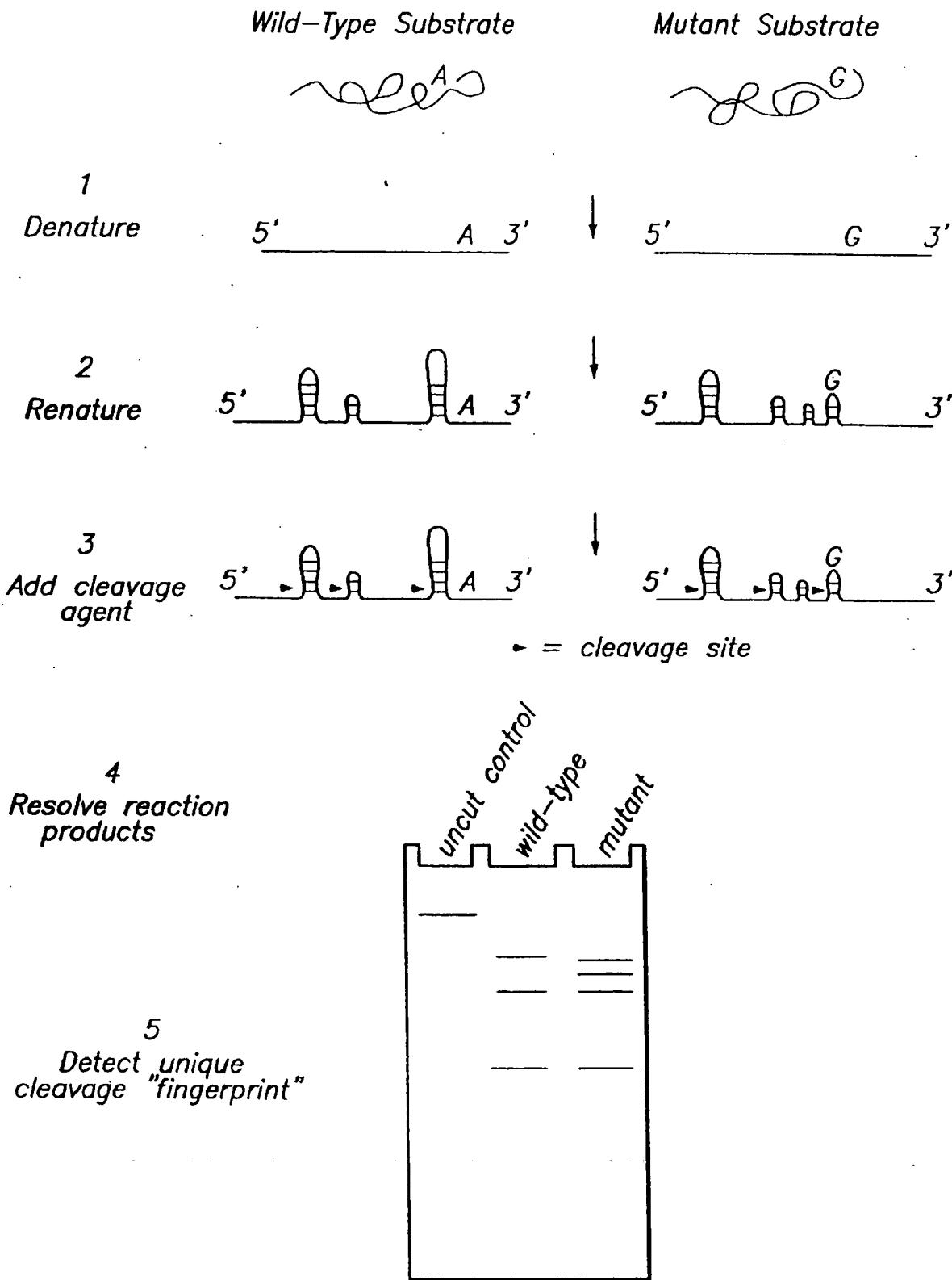


FIG. 29

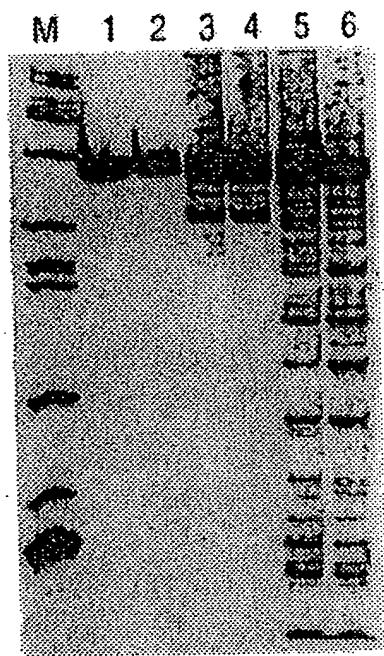


FIG. 30

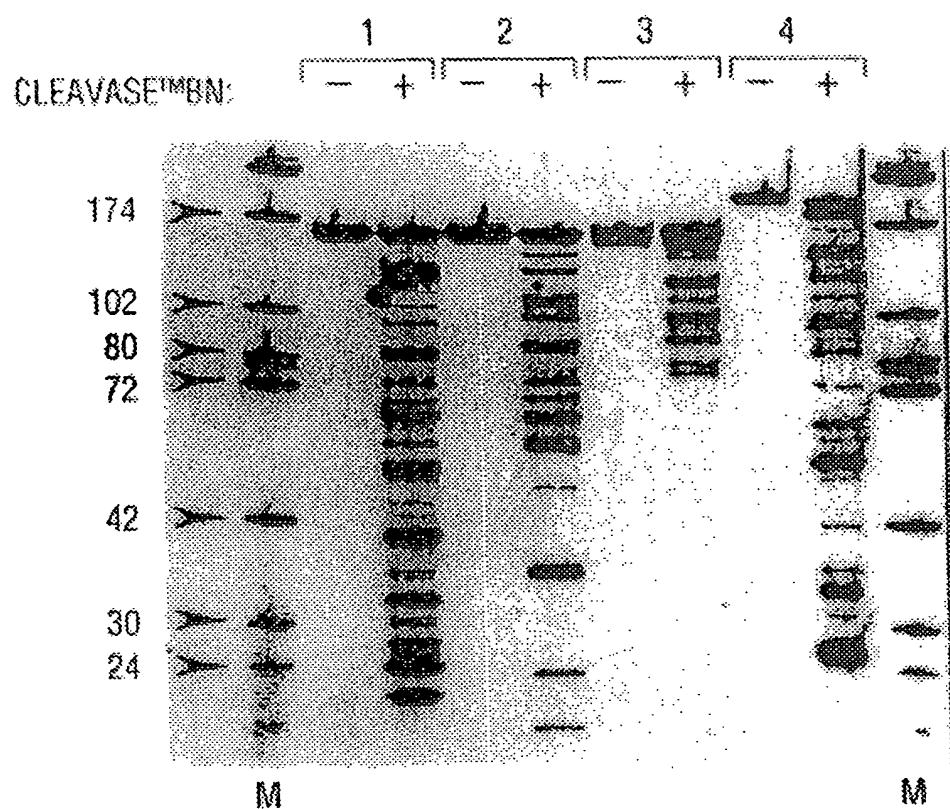


FIG. 31

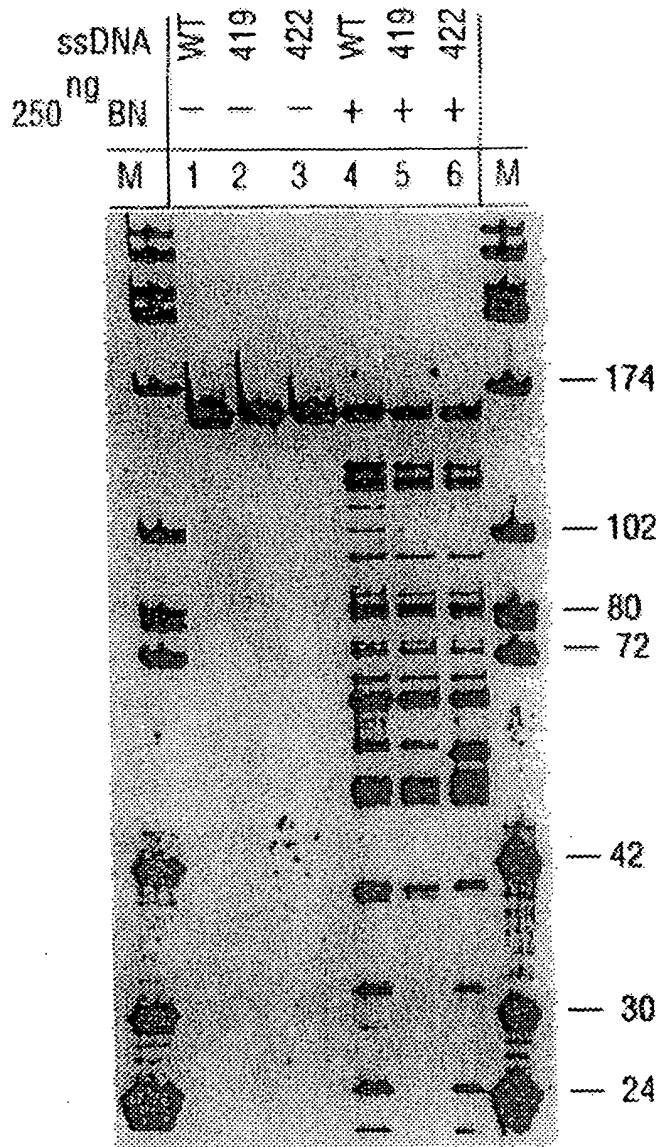


FIG. 32

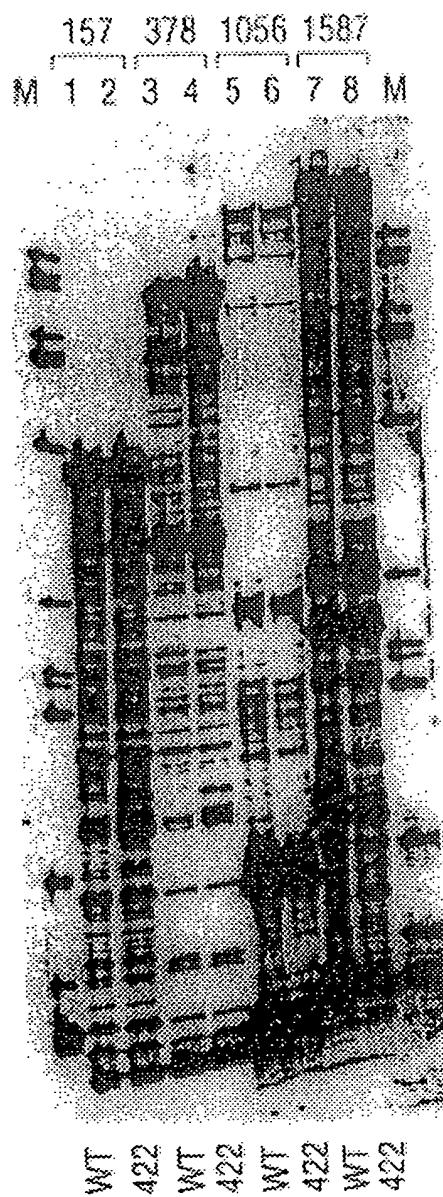


FIG. 33

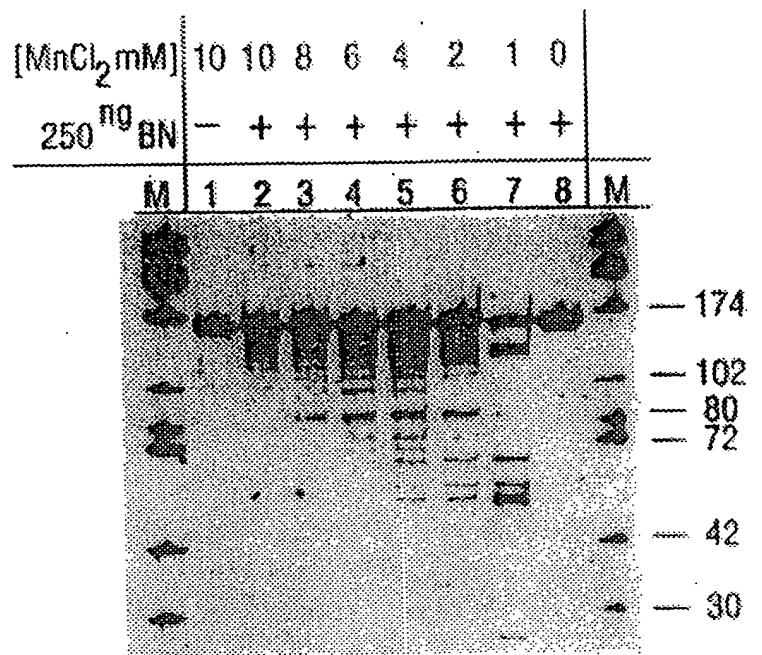


FIG. 34

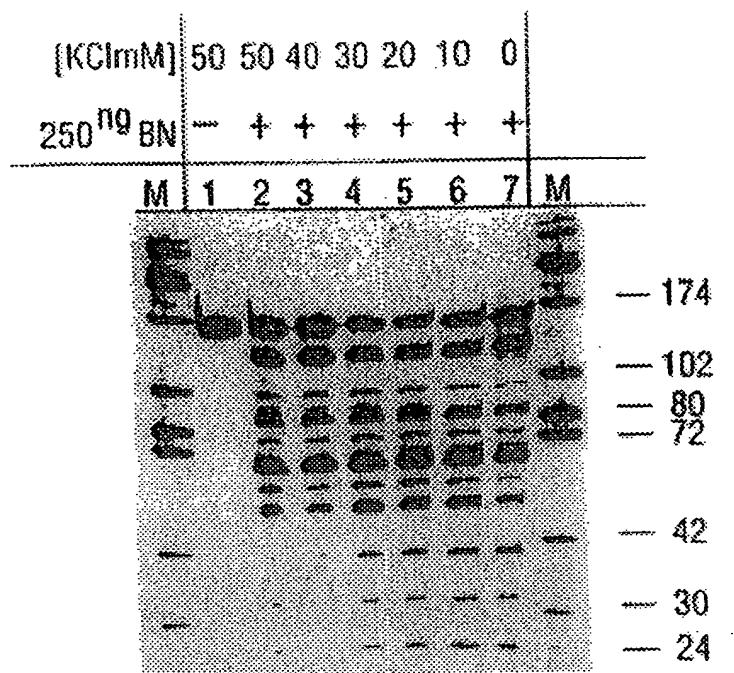


FIG. 35

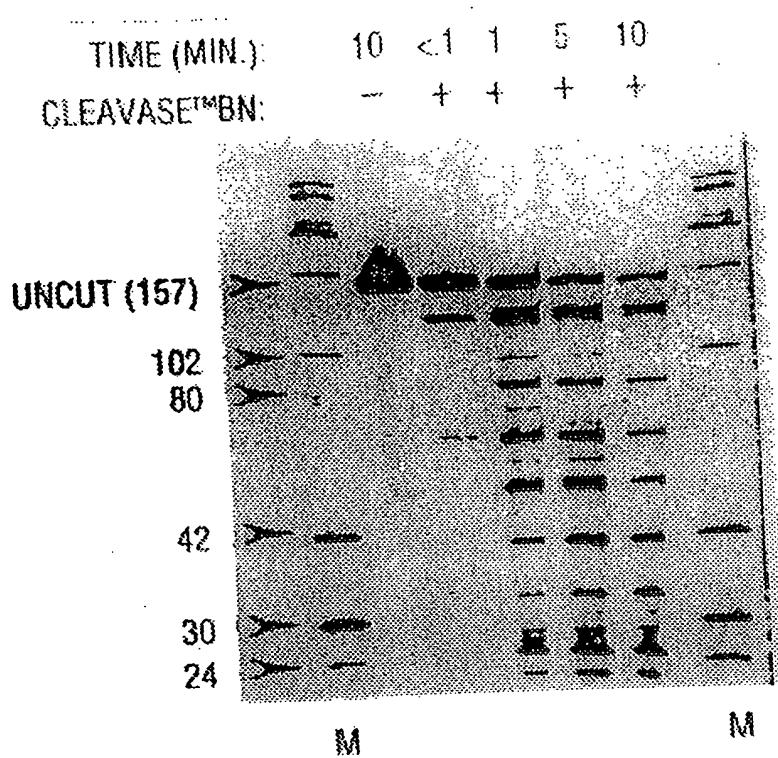


FIG. 36

TEMPERATURE (°C)

55 80 55 60 65 70 75 80

CLEAVASETRON: - - + + + + - +

UNCUT (157)

102

80

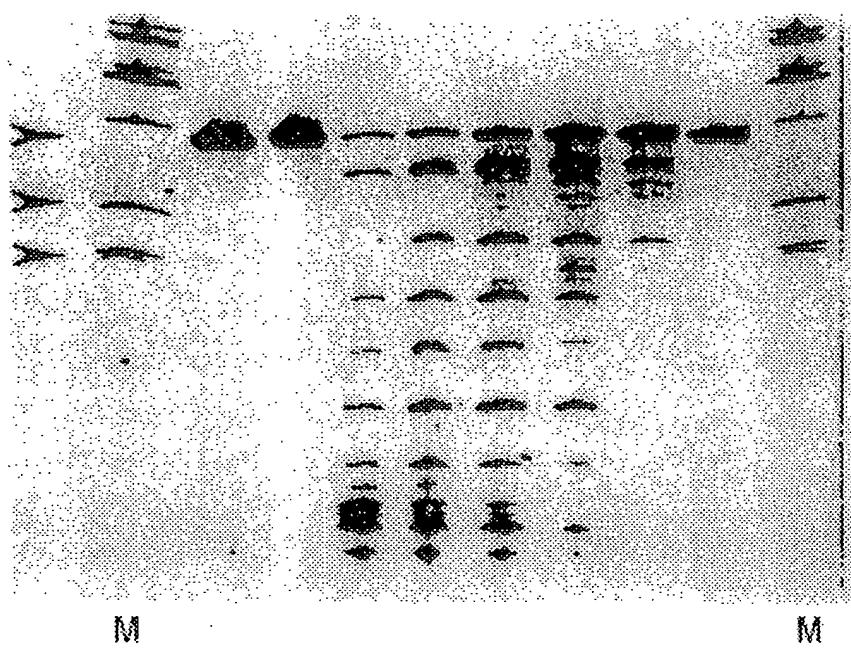


FIG. 37

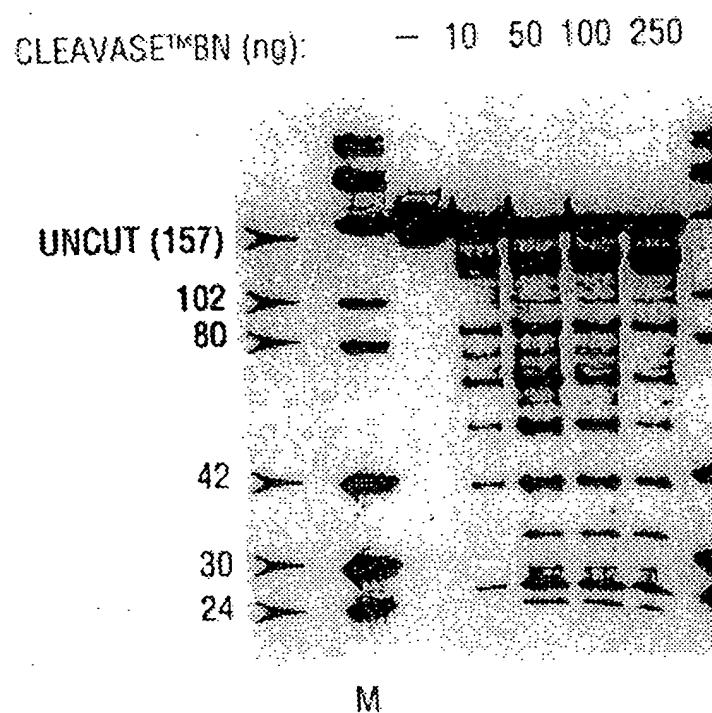


FIG. 38

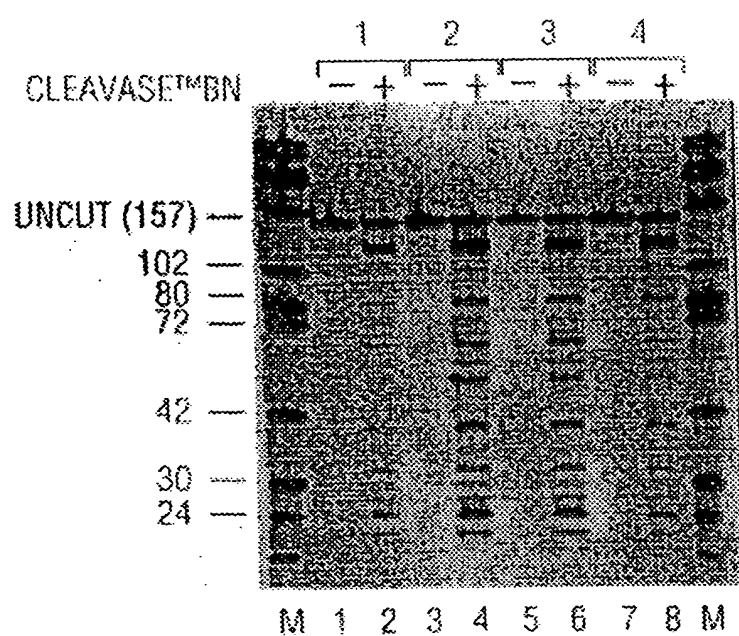


FIG. 39

STRAND	5' - BIOTIN SENSE STRAND				5' - FLUORESCIN ANTI-SENSE STRAND							
	WT	419	422	WT	419	422	WT	419	422			
250 ng BN	-	-	-	+	+	+	+	+	-			
M	1	2	3	4	5	6	7	8	9	10	11	12

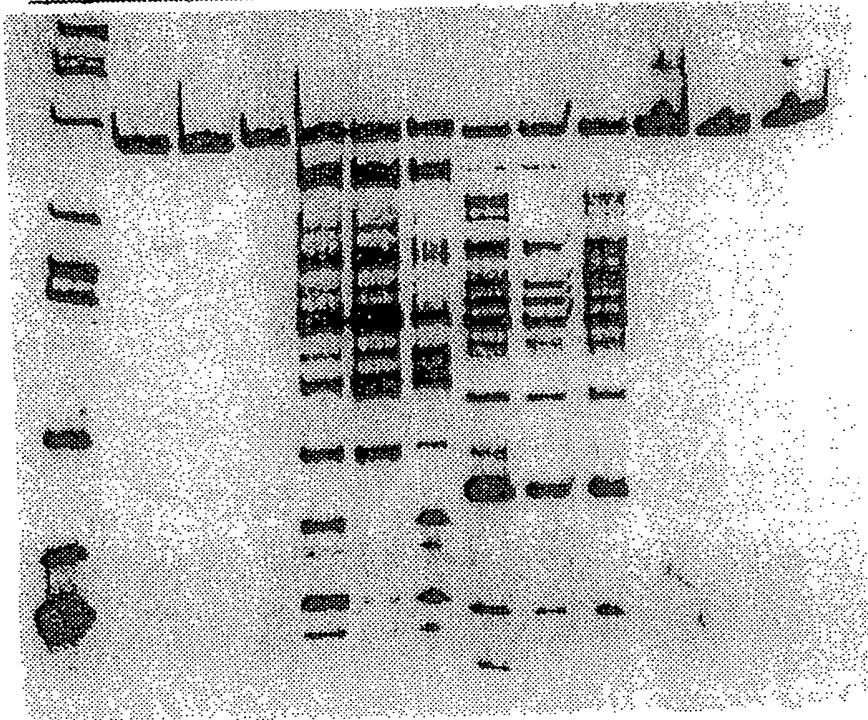


FIG. 40

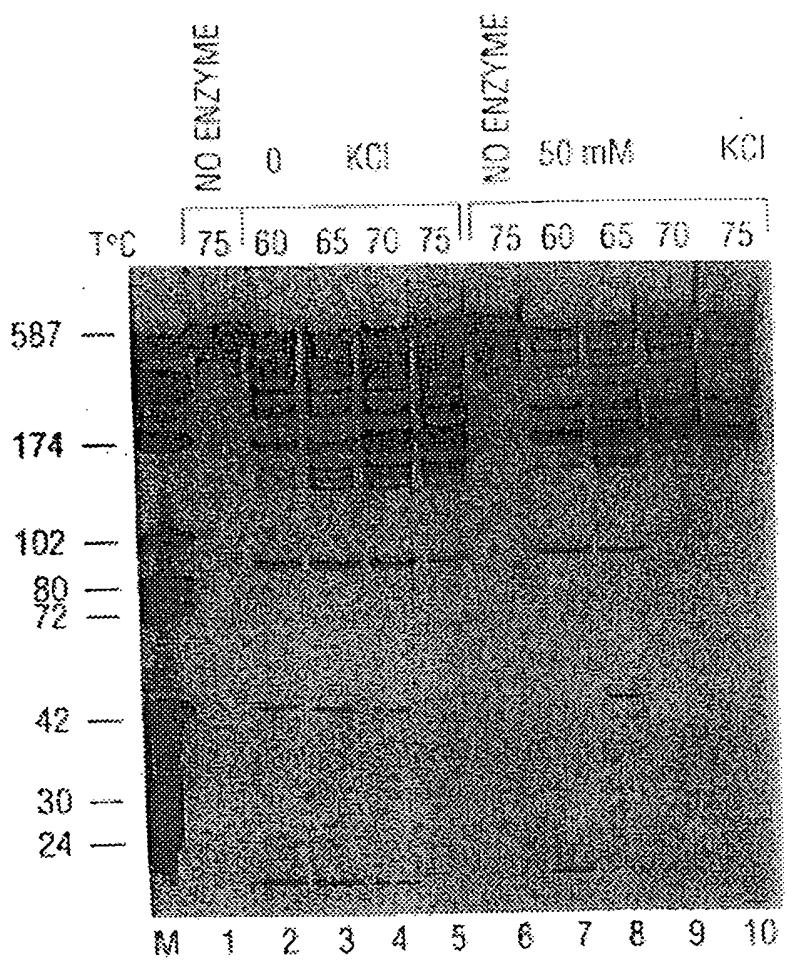


FIG. 41

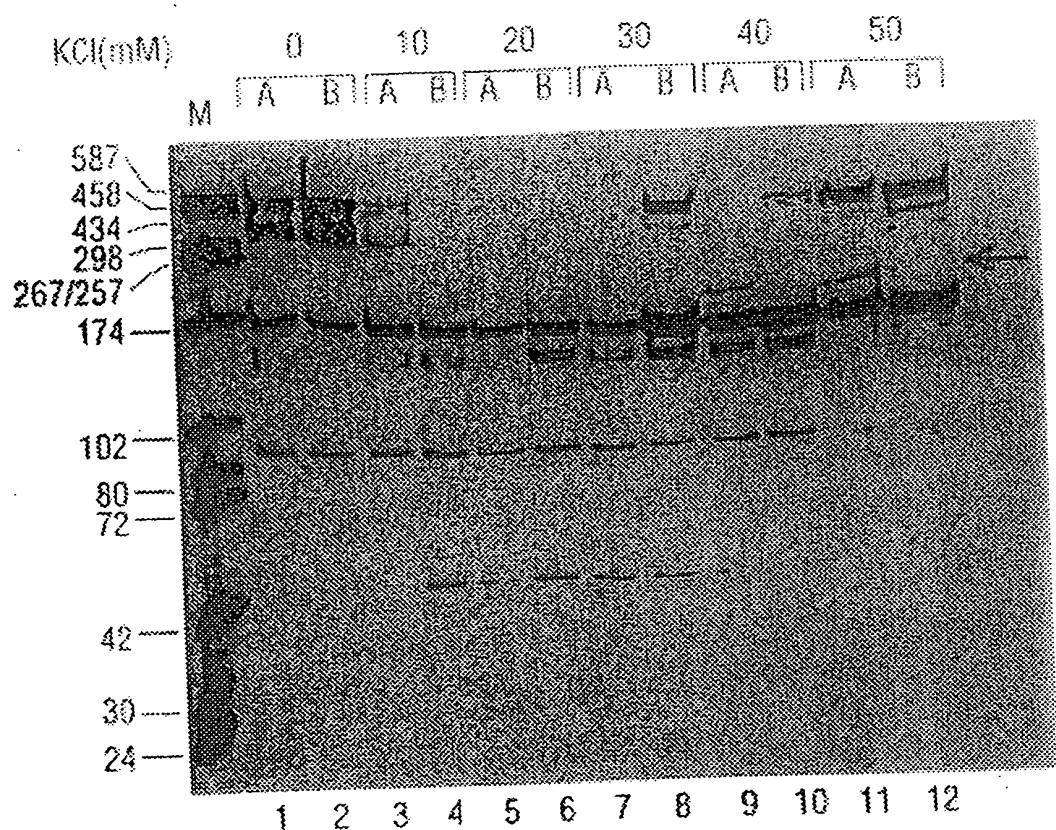


FIG. 42

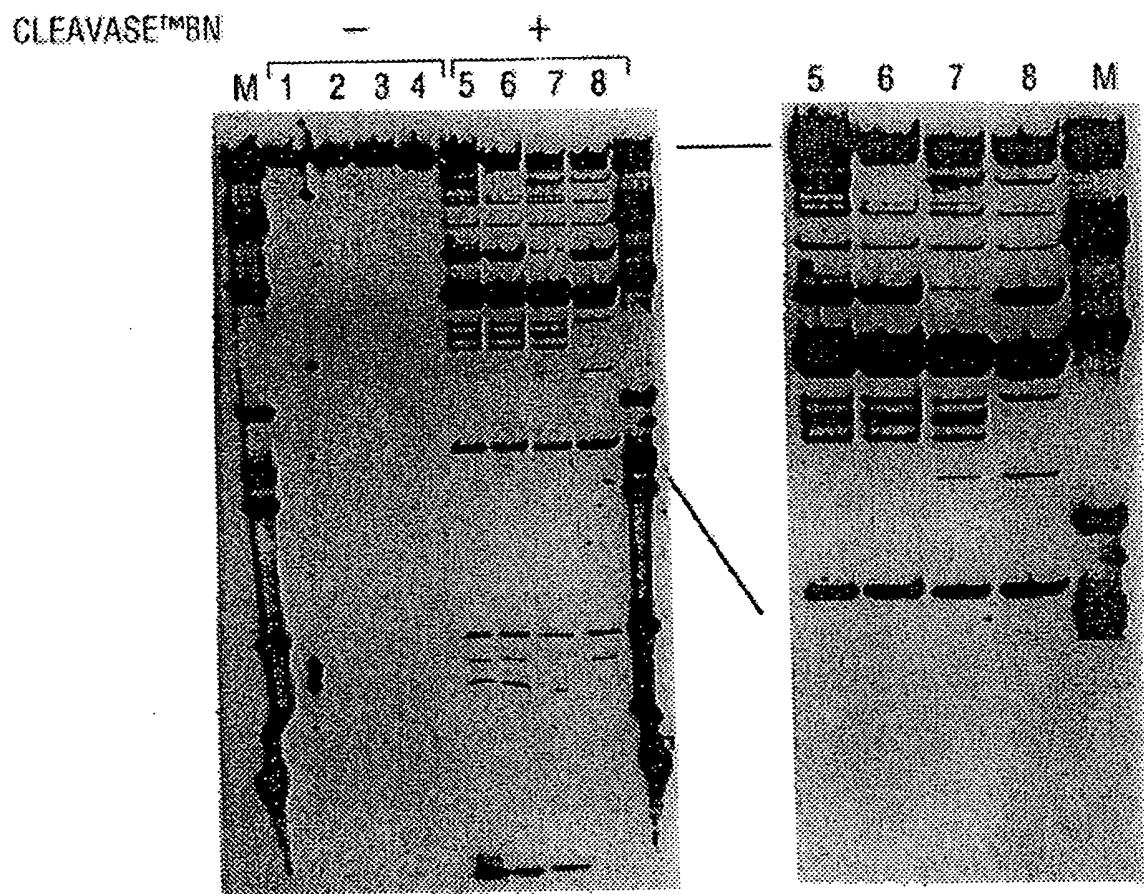


FIG. 43

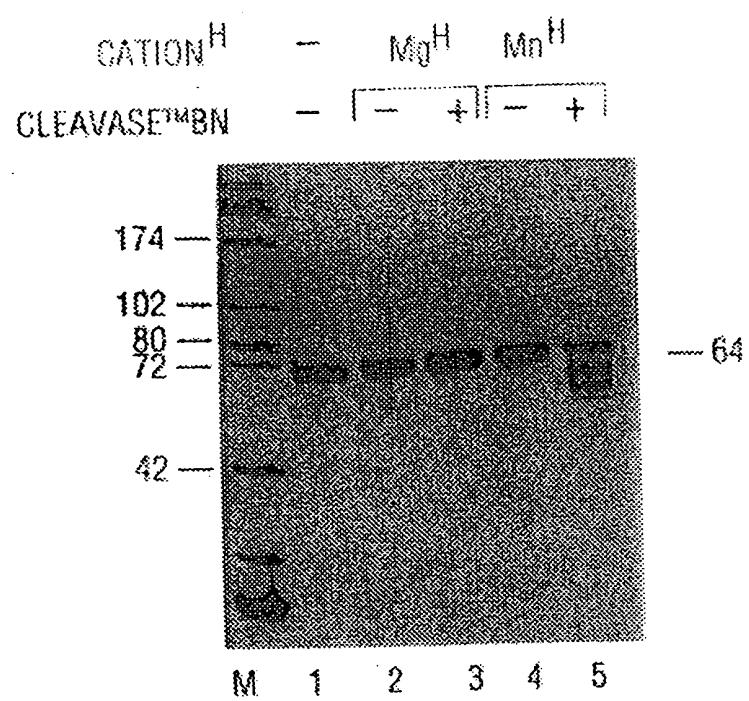


FIG. 44

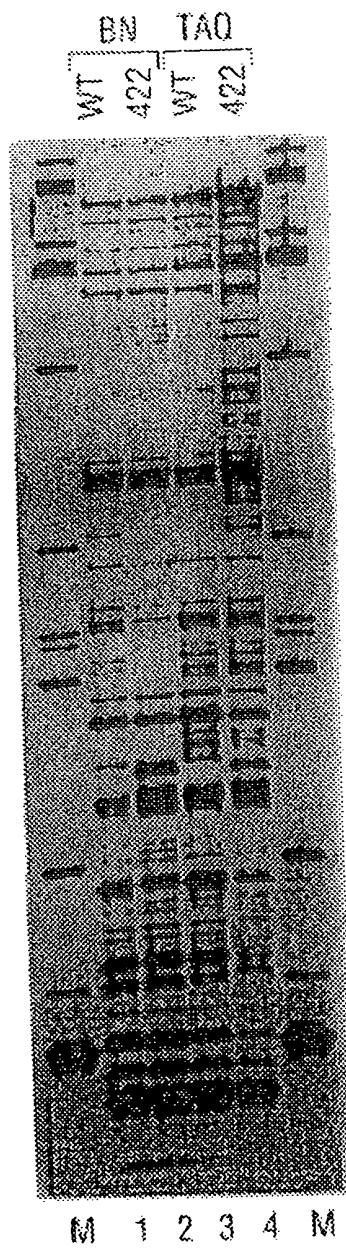


FIG. 45

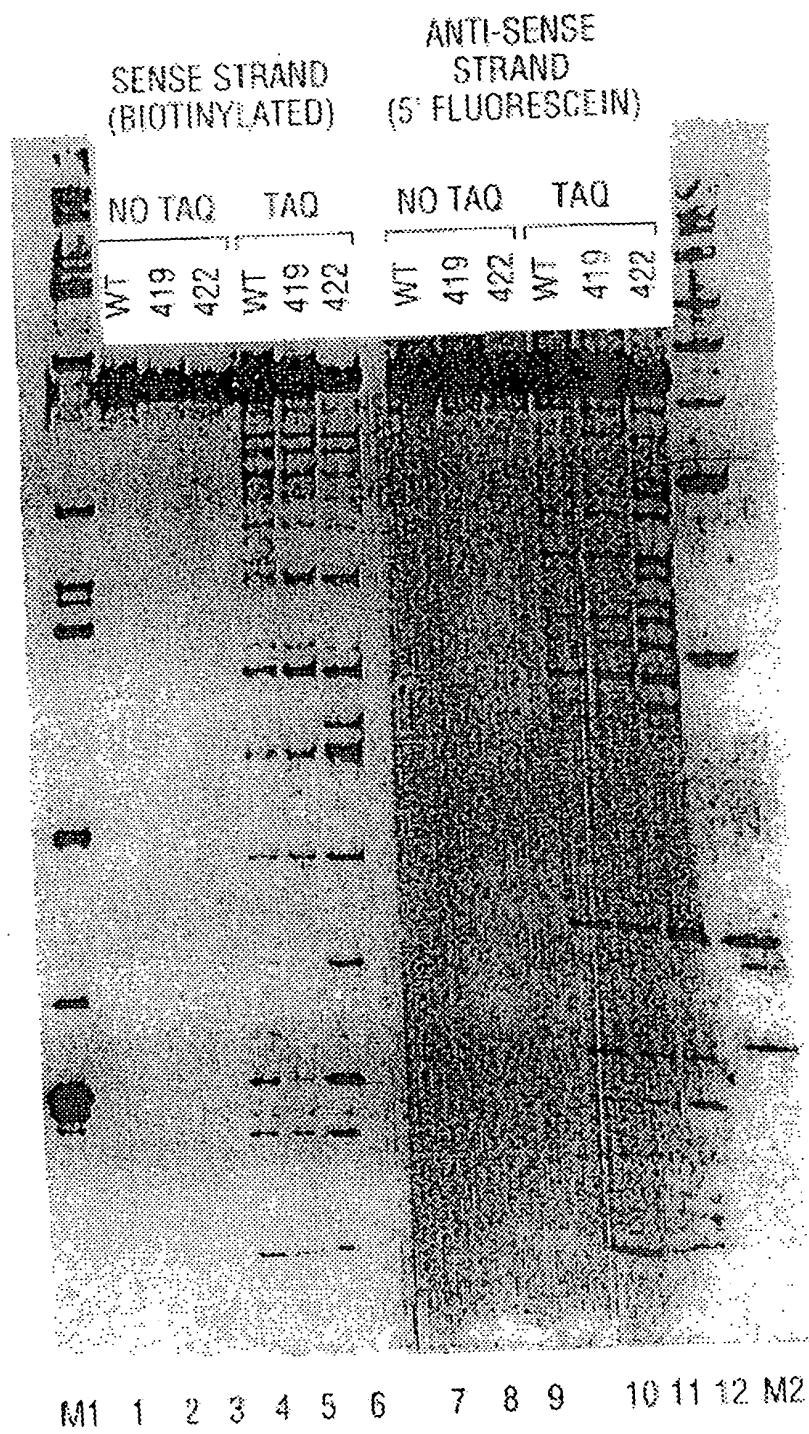


FIG. 46

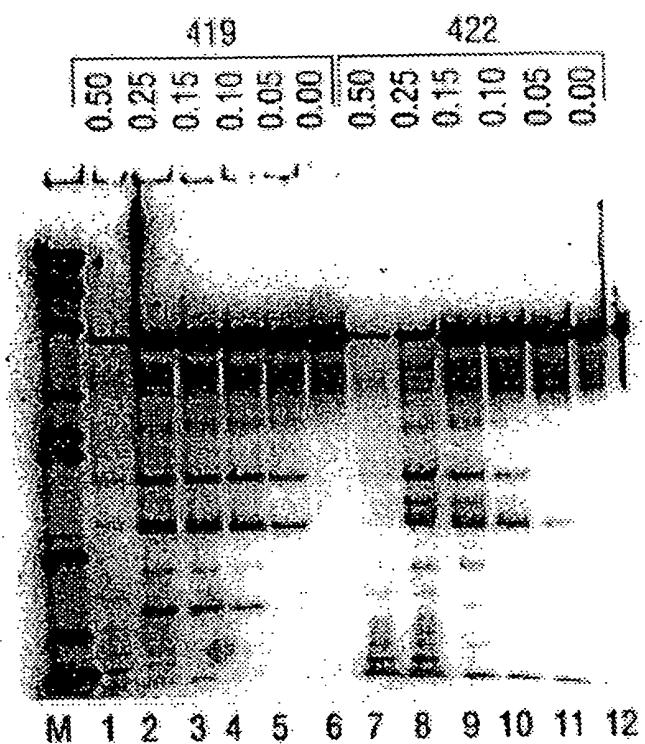


FIG. 47

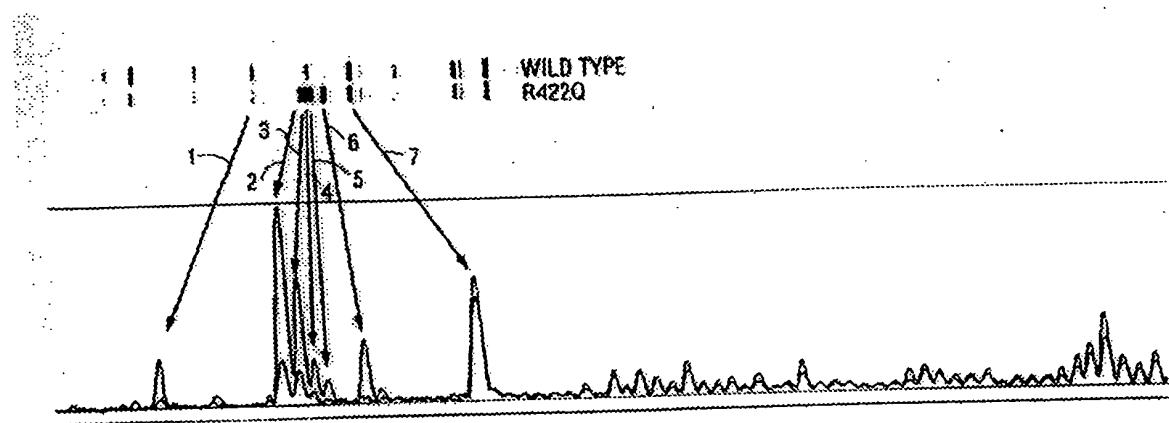


FIG. 48

FIG. 49A

50
L.100.8-1 5'GGCTGACAAGGAAACTCGCTGAGACAGCAGGGACTTTCCACAAAGGGG
(SEQ ID NO: 76) 3'CCGACTGTTCTTCTTGAAGGTGTTCccc

L.46.16-10 5'GGCTGACAAGGAAACTCGCTGAGATAGCAGGGACTTTCCACAAAGGGG
(SEQ ID NO: 77) 3'CCGACTGTTCTTCTTGAAGGTGTTCccc

L.46.16-12 5'GGCTGACAAGGAAACTCGCTGAGATAGCAGGGACTTTCCACAAAGGGG
(SEQ ID NO: 78) 3'CCGACTGTTCTTCTTGAAGGTGTTCccc

L.19.16-3 5'GGCTGACAAGGAAACTCGCTGAGACAGCAGGGACTTTCCACAAAGGGG
(SEQ ID NO: 79) 3'CCGACTGTTCTTCTTGAAGGTGTTCccc

L.CEM/251 5'GGCTGACAAGGAAACTCGCTGAAACAGCAGGGACTTTCCACAAAGGGG
(SEQ ID NO: 80) 3'CCGACTGTTCTTCTTGAAGGTGTTCccc

L.36.8-3 5'GGCTGACAAGGAAACTCGCTGAGACAGCAGGGACTTTCCACAAAGGGG
(SEQ ID NO: 81) 3'CCGACTGTTCTTCTTGAAGGTGTTCccc

FIG. 49B

L.100.8-1
(SEQ ID NO: 76)
ATGTTACGGGAGGTACTGGGGAGGGCCGGTGGGAACCCCCACTCTCT
TACAATGCCCTCCATGACCCCTCCTGGCCAGCCCC
100

L.46.16-10
(SEQ ID NO: 77)
ATGTTATGGGAGG-----AGCCGGTCCGGGAACACCCACTTTCT
TACAATAACCCCTCC-----TCGGCCAGCCCC
ATGTTATGGGAGG-----AGCCGGTCCGGGAACACCCACTTTCT
TACAATAACCCCTCC-----TCGGCCAGCCCC
ATGTTACGGGAGGTACTGGGGAGGGCCGGTGGGAACCCCCACTCTCT
TACAATGCCCTCCATGACCCCTCCTGGCCAGCCCC
ATGTTACGGGAGGTACTGGGAAGGGCCGGTGGGAACCCCCACTCTCT
TACAATGCCCTCCATGACCCCTCCTGGCCAGCCCC
ATGTTACGGGAGGTACTGGGGAGGGCCGGTGGGAACCCCCACTCTCT
TACAATGCCCTCCATGACCCCTCCTGGCCAGCCCC
L.36.8-3
(SEQ ID NO: 81)
ATGTTACGGGAGGTACTGGGGAGGGCCGGTGGGAACCCCCACTCTCT
TACAATGCCCTCCATGACCCCTCCTGGCCAGCCCC

L . 100 . 8 - 1	5' TGATGTATAAATATCACTGCATTTCGCTCTGTATTCA GT CAGT CAGC GAGA C G G A 3' ACTACATATTAGTGACGTAAAGCGAGACATAAGTCA GGAGACGGCT
L . 46 . 16 - 10	5' TGATGTATAAATATCACTGCATTTCGCTCTGTATTCA GT CAGT CAGC GAGA C G G A 3' ACTACATATTAGTGACGTAAAGCGAGACATAAGTCA GGAGACGGCT
L . 46 . 16 - 12	5' TGGTGTATAAATATCACTGCATTTCGCTCTGTATTCA GT CAGT CAGC GAGA C G G A 3' ACCACATATTAGTGACGTAAAGCGAGACATAAGTCA GGAGACGGCT
L . 19 . 16 - 3	5' TGATGTATAAATATCACTGCATTTCGCTCTGTATTCA GT CAGT CAGC GAGA C G G A 3' ACTACATATTAGTGACGTAAAGCGAGACATAAGTCA GGAGACGGCT
L . CEM / 251	5' TGATGTATAAATATCACTGCATTTCGCTCTGTATTCA GT CAGT CAGC GAGA C G G A 3' ACTACATATTAGTGACGTAAAGCGAGACATAAGTCA GGAGACGGCT
L . 36 . 8 - 3	5' TGATGTATAAATATCACTGCATTTCGCTCTGTATTCA GT CAGT CAGC GAGA C G G A 3' ACTACATATTAGTGACGTAAAGCGAGACATAAGTCA GGAGACGGCT

FIG. 49C

L . 100 . 8 - 1	GAGGCTGGCAGATTGAGCCCTGGAGGTTCTCCAGGCACTAGCAGCTTAGCTCCGACCGTCAACTCGGGACCCTCCAAGAGGGTGGATCGTCATC
L . 46 . 16 - 10	GAGGCTGGCAGATTGAGCCCTGGAGGTTCTCCAGGCACTAGCAGGTAGCTCCGACCGTCTAACTCGGGACCCTCCAAGAGGGTGGATCGTCATC
L . 46 . 16 - 12	GAGGCTGGCAGATTGAGCCCTGGAGGTTCTCCAGGCACTAGCAGGTAGCTCCGACCGTCTAACTCGGGACCCTCCAAGAGGGTGGATCGTCATC
L . 19 . 16 - 3	GAGGCTGGCAGATTGAGCCCTGGAGGTTCTCCAGGCACTAGCAGGTAGCTCCGACCGTCTAACTCGGGACCCTCCAAGAGGGTGGATCGTCATC
L . CEM / 251	GAGGCTGGCAGATTGAGCCCTGGAGGTTCTCCAGGCACTAGCAGGTAGCTCCGACCGTCTAACTCGGGACCCTCCAAGAGGGTGGATCGTCATC
L . 36 . 8 - 3	GAGGCTGGCAGATTGAGCCCTGGAGGTTCTCCAGGCACTAGCAGGTAGCTCCGACCGTCTAACTCGGGACCCTCCAAGAGGGTGGATCGTCATC

FIG. 49D

L: 100. 8 -1 5' AGCCCTGGGT GTTCCCTGCTAGACTCTCACCAAGC
 (SEQ ID NO: 76) 3' TCGGACCCACAAGGACCATTCTGAAGTGGTCA

 L: 46.16-10 5' AGCCCTGGGT GTTCCCTGCTAGACTCTCACCAAGC
 (SEQ ID NO: 77) 3' TCGGACCCACAAGGACCATTCTGAAGTGGTCA

 L: 46.16-12 5' AGCCCTGGGT GTTCCCTGCTAGACTCTCACCAAGC
 (SEQ ID NO: 78) 3' TCGGACCCACAAGGACCATTCTGAAGTGGTCA

 L: 19.16-3 5' AGCCCTGGGT GTTCCCTGCTAGACTCTCACCAAGC
 (SEQ ID NO: 79) 3' TCGGACCCACAAGGACCATTCTGAAGTGGTCA

 L: CEM/251 5' AGCCCTGGGT GTTCCCTGCTAGACTCTCACCAAGC
 (SEQ ID NO: 80) 3' TCGGACCCACAAGGACCATTCTGAAGTGGTCA

 L: 36.8-3 5' AGCCCTGAGTGGTCCCTGCTAAACTCTCACCAAGC
 (SEQ ID NO: 81) 3' TCGGACCTACAAGGACGATTTGAGTGGTCA

HAIRPIN

FIG. 49E

L. 100. 8 -1
 (SEQ ID NO: 76) 300
 CAGAGTGGCTCCACGCCCTGCTTAAGACCTCTTCATAAAAGCTGCC
 GTCTCAQCGAGGTGCCAACGAATTCTGGAGAAGTTTCTGACGG

 L. 46.16-10
 (SEQ ID NO: 77)
 CAGAGTGGCTCCACGCCCTGCTTAAGACCTCTTCATAAAAGCTGCC
 GTCTCAQCGAGGTGCCAACGAACGAATTCTGGAGAAGTTTCTGACGG

 L. 46.16-12
 (SEQ ID NO: 78)
 CAGAGTGGCTCCACGCCCTGCTTAAGACCTCTTCATAAAAGCTGCC
 GTCTCAQCGAGGTGCCAACGAACGAATTCTGGAGAAGTTTCTGACGG

 L. 19.16-3
 (SEQ ID NO: 79)
 CAGAGTGAATCCACGCCCTGCTTAAGACCTCTTCATAAAAGCTGCC
 GTCTCACTGAGGTGCCAACGAACGAATTCTGGAGAAGTTTCTGACGG

 L. CEM/251
 (SEQ ID NO: 80)
 CAGAGGCTCCACGCCCTGCTTAAGACCTCTTCATAAAAGCTGCC
 GTCTCGGCAGGGTGGCAACGAACGAATTCTGGAGAAGTTTCTGACGG

 L. 36.8-3
 (SEQ ID NO: 81)

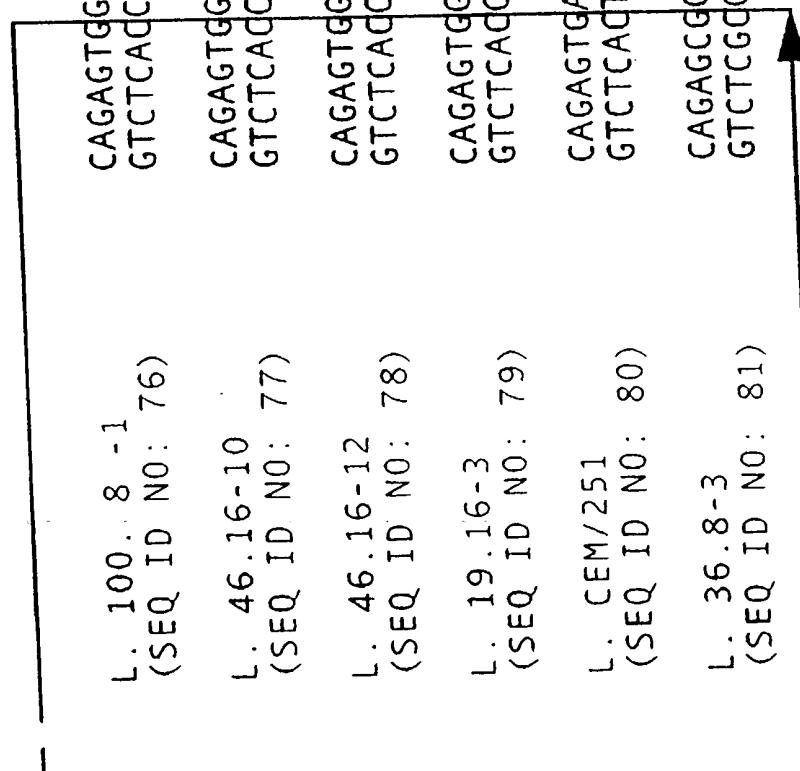


FIG. 49F

L . 100 . 8 - 1	5' ATTTTTAGAAGTAGGCCAAGTGTGTTCCCATTCTCTCTAGCCCCGGCCCTG 3' TAAATCTTCATCGGTACACACAAGGTAGAGGATGGGGAC	G 3' C 5'	350
L . 46 , 16 - 10	5' ATTTTAGAAGTAAGCCAAAGTGTGTTCCCATTCTCTCTAGCCCCGGCCCTG 3' TAAATCTTCATCGGTACACACAAGGTAGAGGATGGGGAC	G 3' C 5'	
L . 46 . 16 - 12	5' ATTTTAGAAGTAAGCCAAAGTGTGTTCCCATTCTCTCTAGCCCCGGCCCTG 3' TAAATCTTCATCGGTACACACAAGGTAGAGGATGGGGAC	G 3' C 5'	
L . 19 , 16 - 3	5' ATTTTAGAAGTAGGCTAGTGTGTTCCCATTCTCTCTAGCCCCGGCCCTG 3' TAAATCTTCATCGGTACACACAAGGTAGAGGATGGGGAC	G 3' C 5'	
L . CEM / 251	5' ATTTTAGAAGCTAGTGTGTTCCCATTCTCTCTAGCCCCGGCCCTG 3' TAAATCTTCATCGGTACACACAAGGTAGAGGATGGGGAC	G 3' C 5'	
L . 36 . 8 - 3	5' ATTTTAGAAGTAGGCTAGTGTGTTCCCATTCTCTCTAGCCCCGGCCCTG 3' TAAATCTTCATCGGTACACACAAGGTAGAGGATGGGGAC	G 3' C 5'	

FIG. 49G



FIG. 50

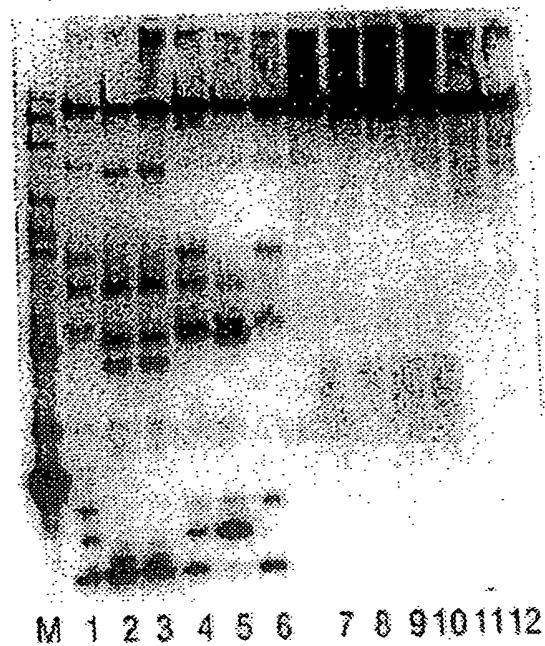


FIG. 51

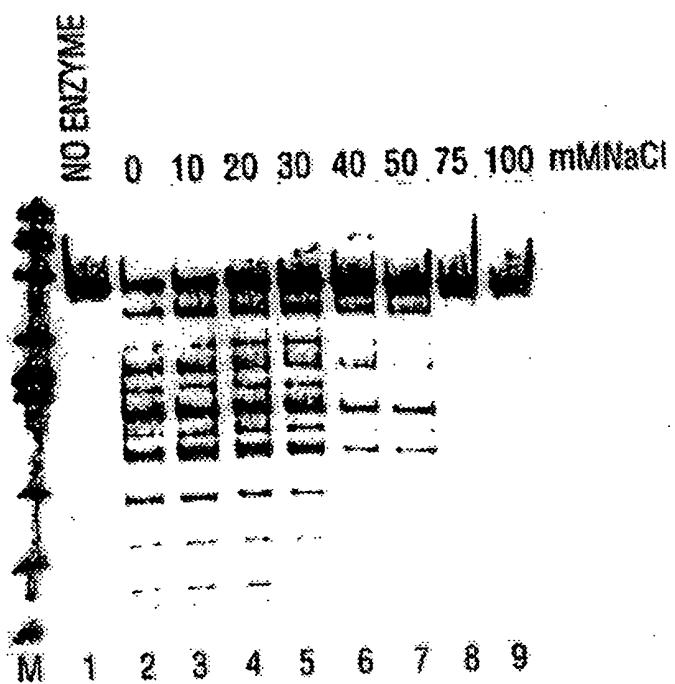


FIG. 52

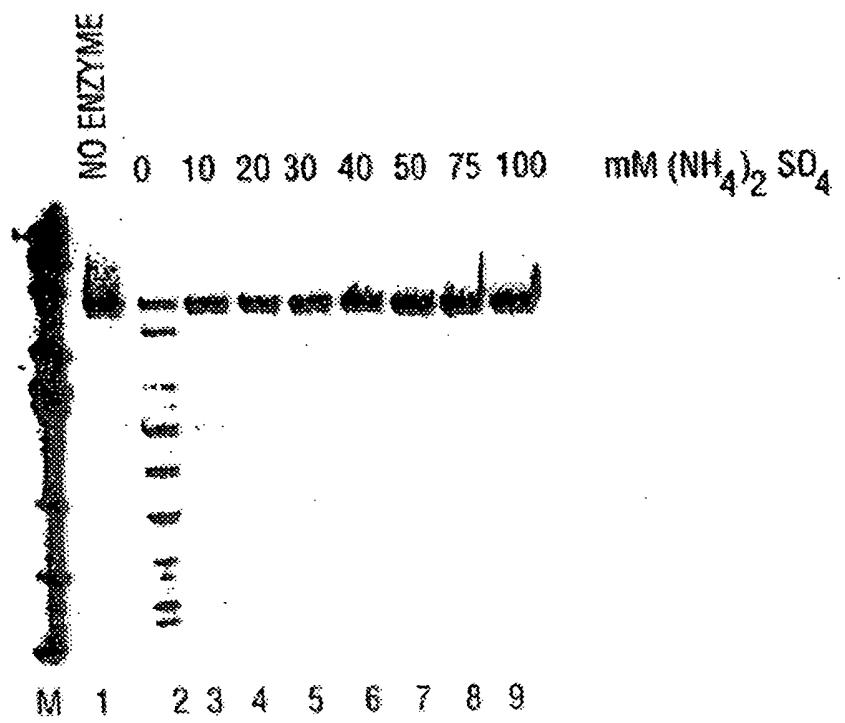


FIG. 53

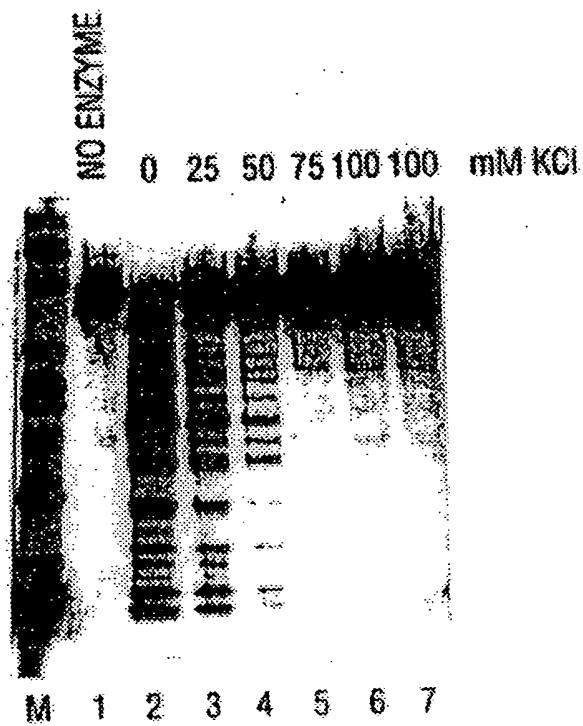


FIG. 54

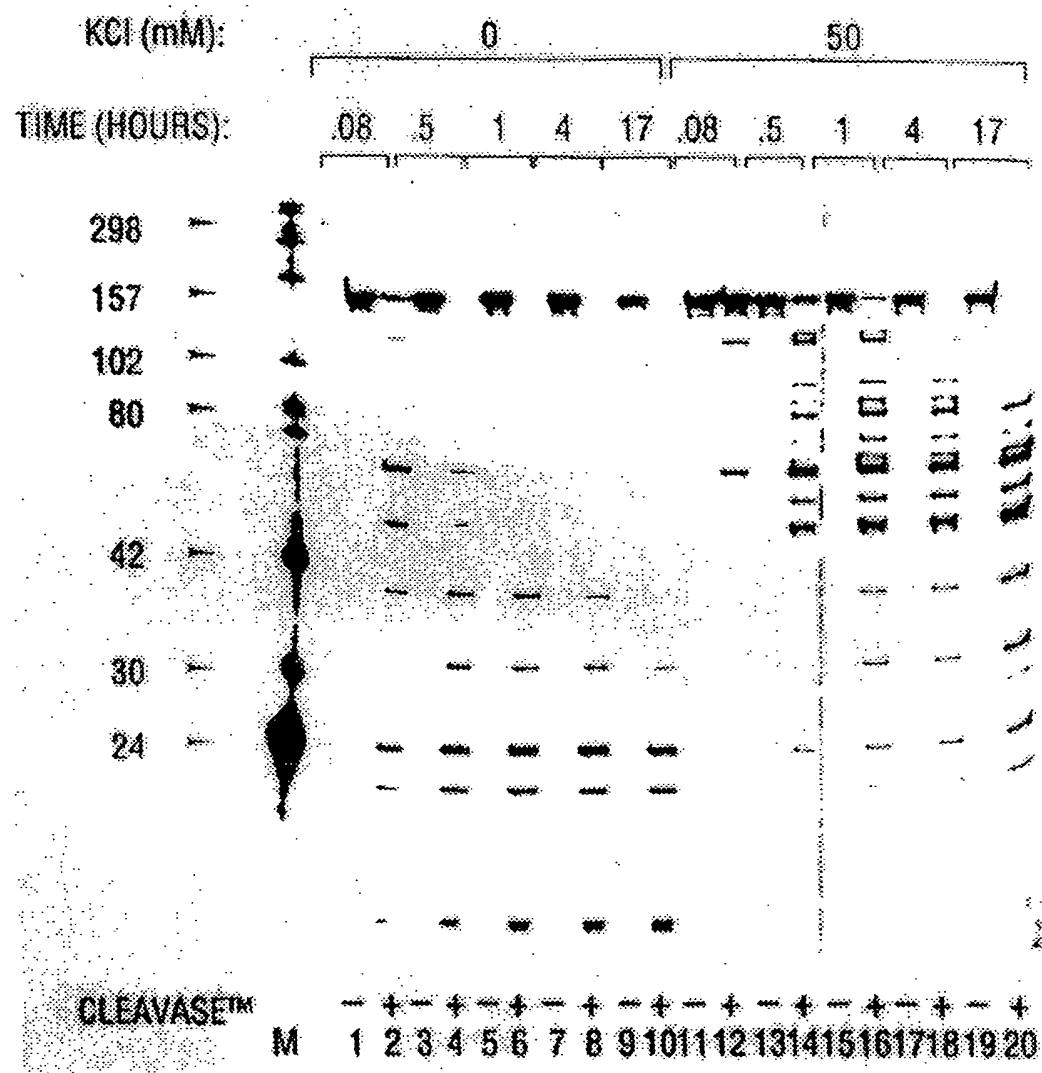


FIG. 55

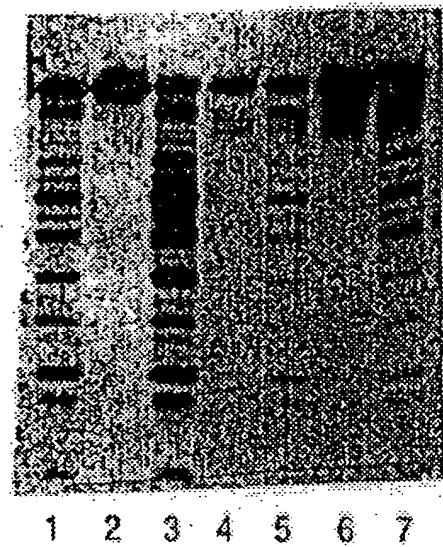


FIG. 56

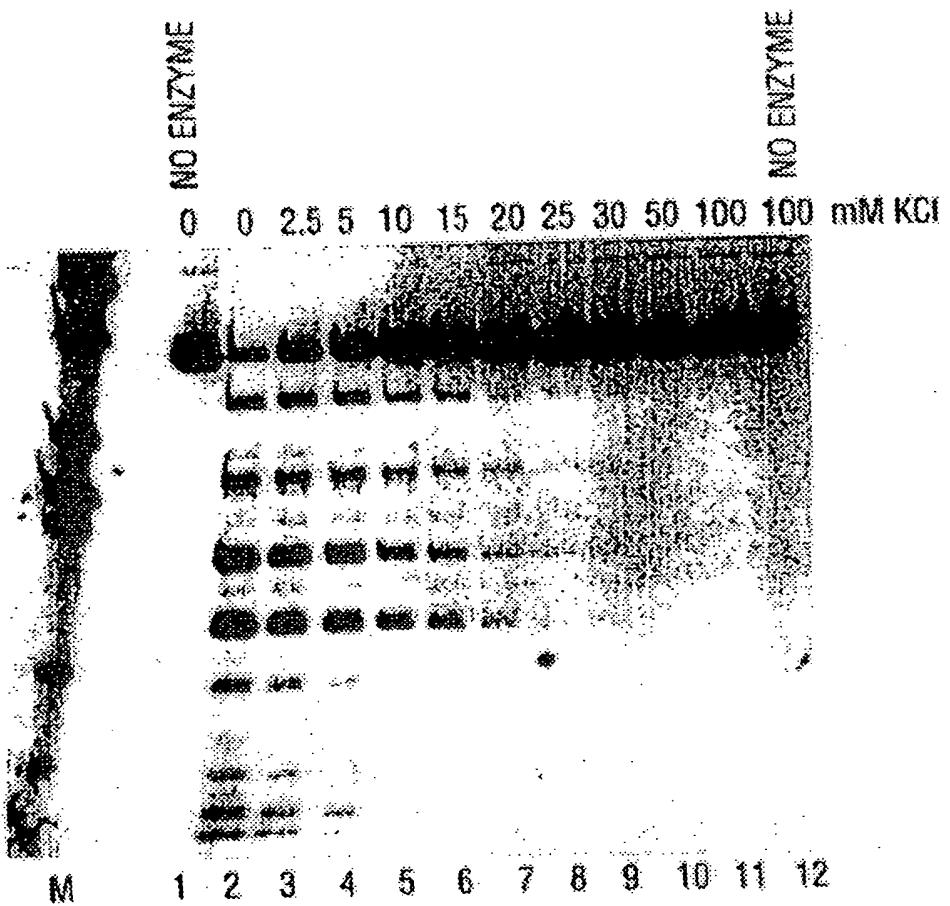


FIG. 57

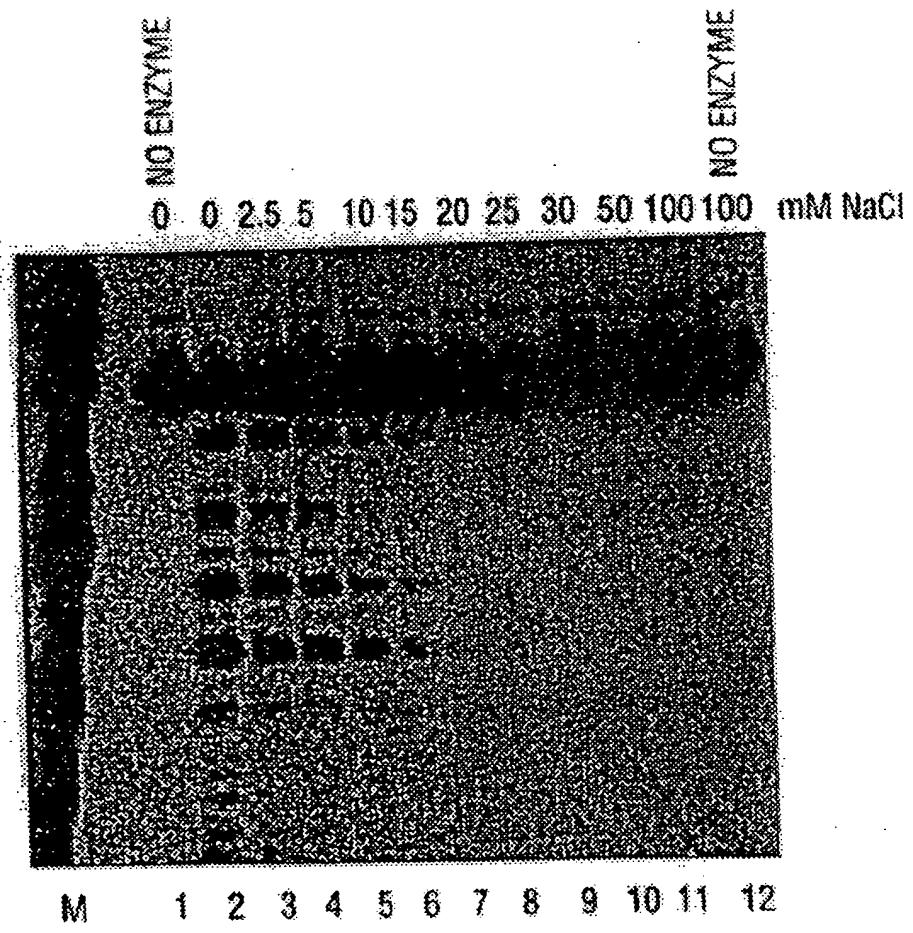


FIG. 58

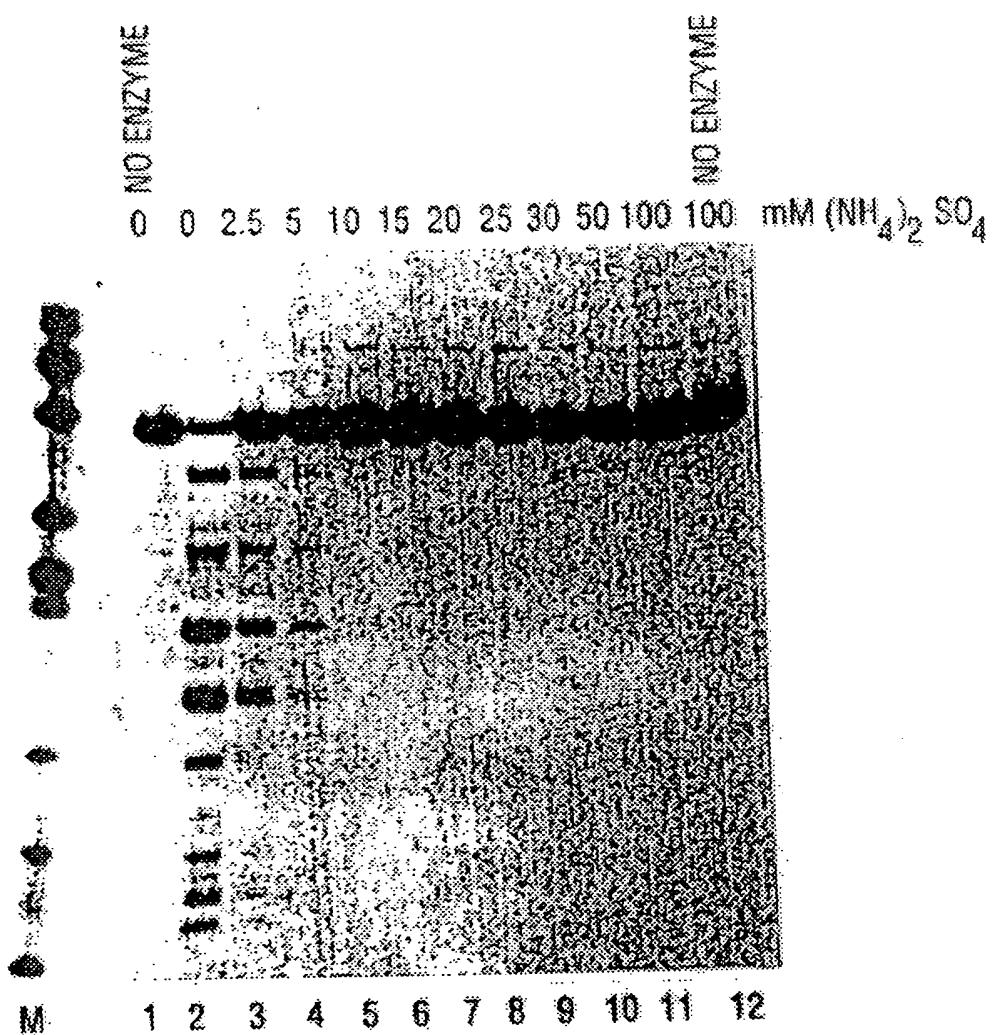


FIG. 59

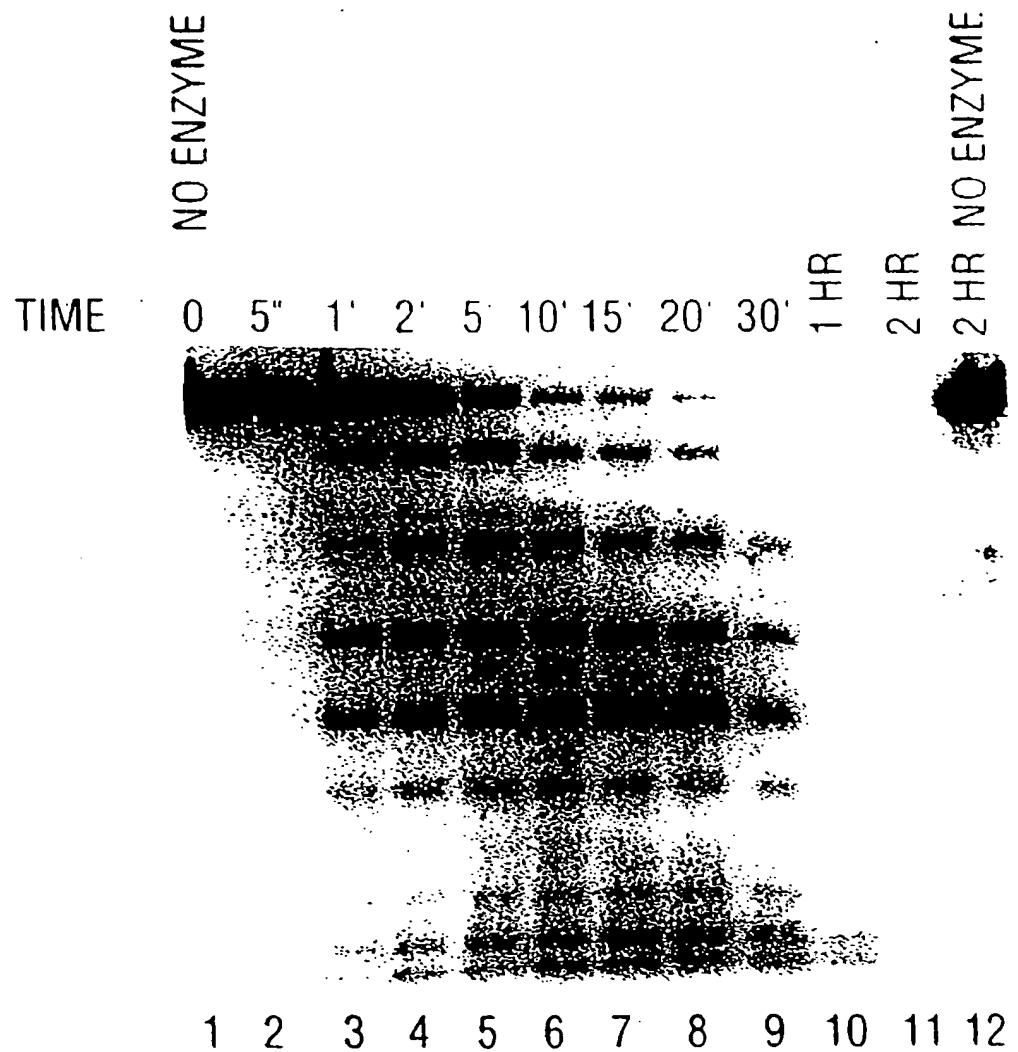


FIG. 60

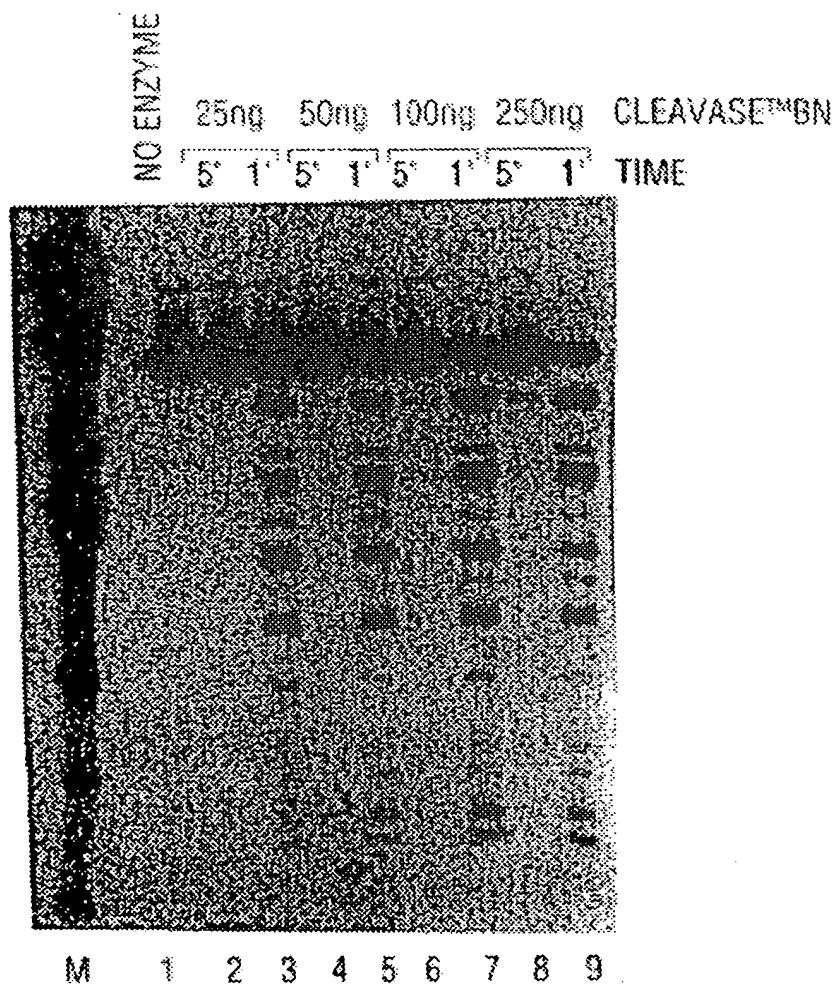


FIG. 61

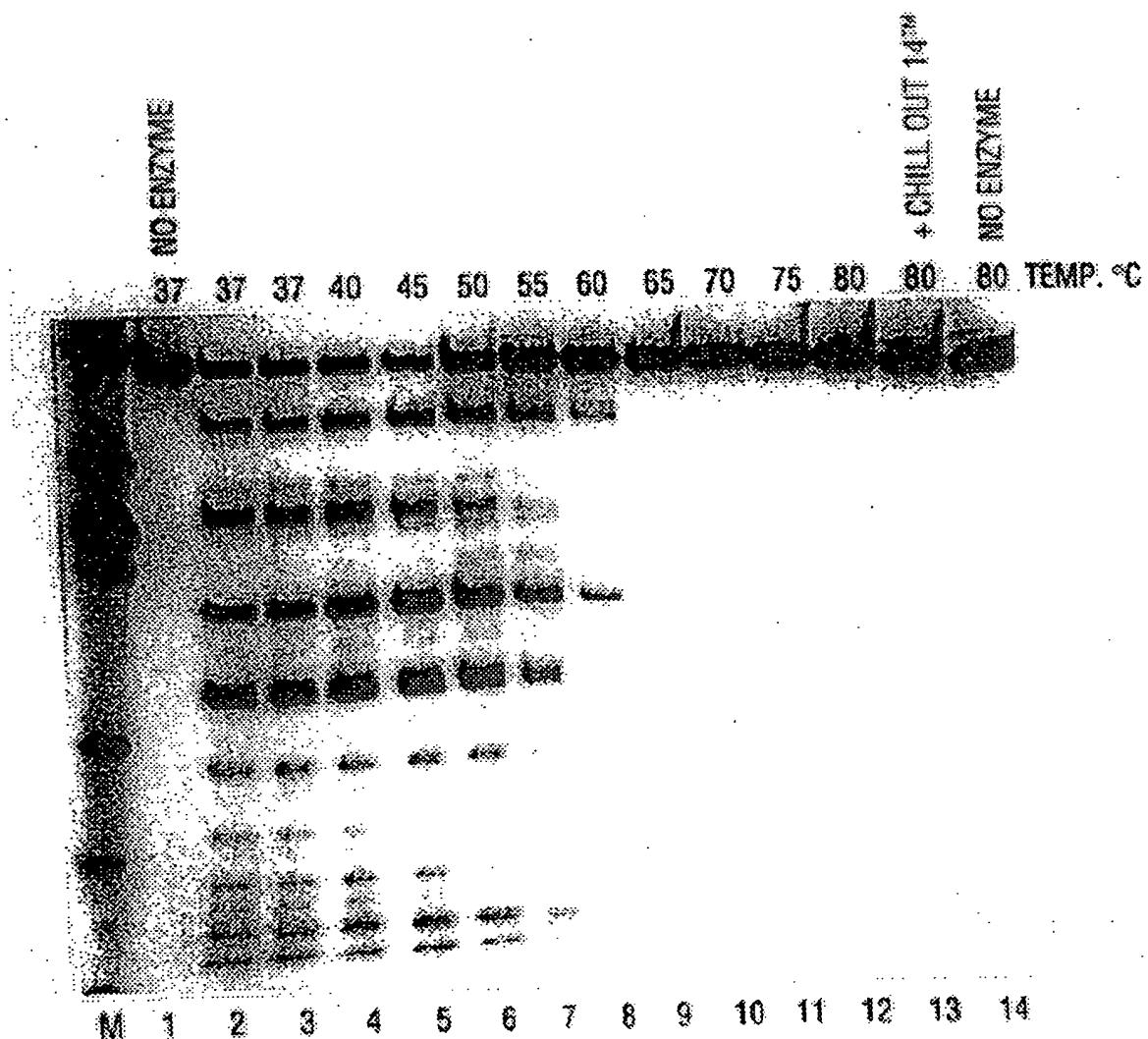


FIG. 62

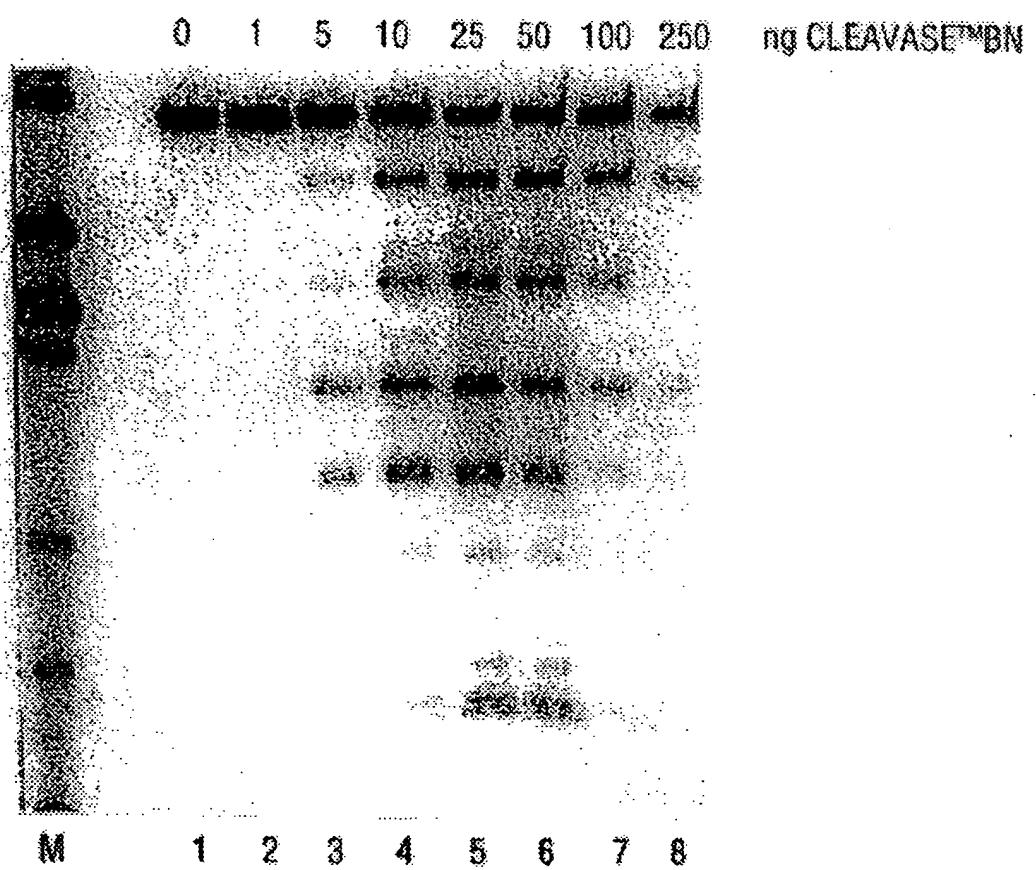


FIG. 63

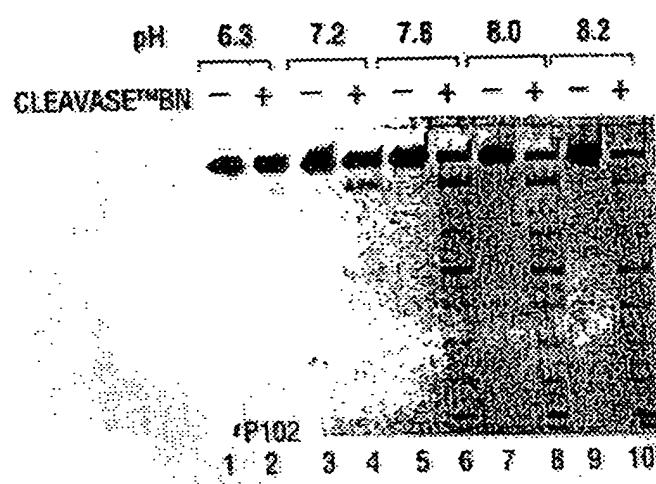


FIG. 64A

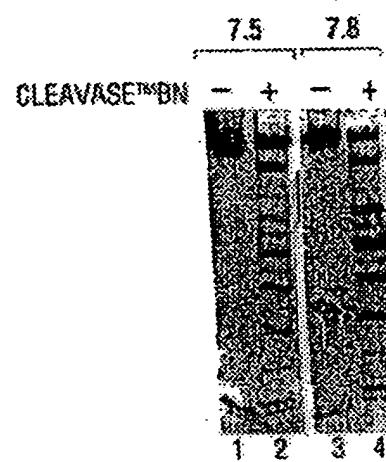


FIG. 64B

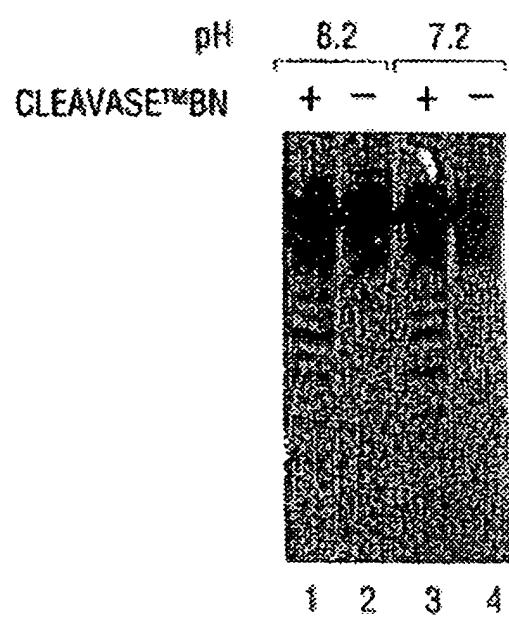


FIG. 65A

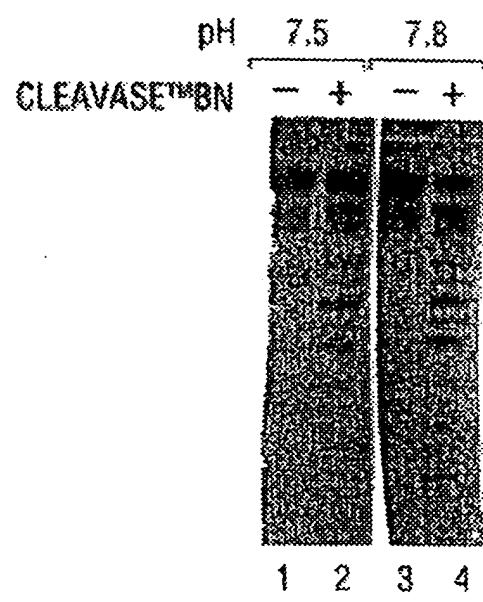


FIG. 65B

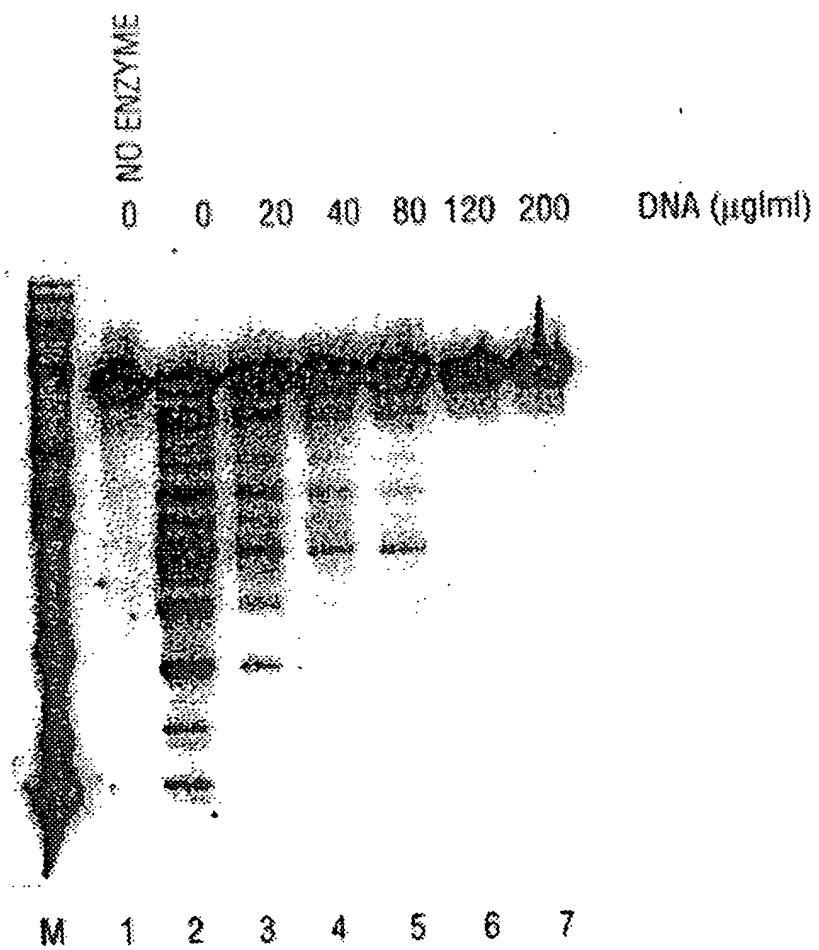


FIG. 66

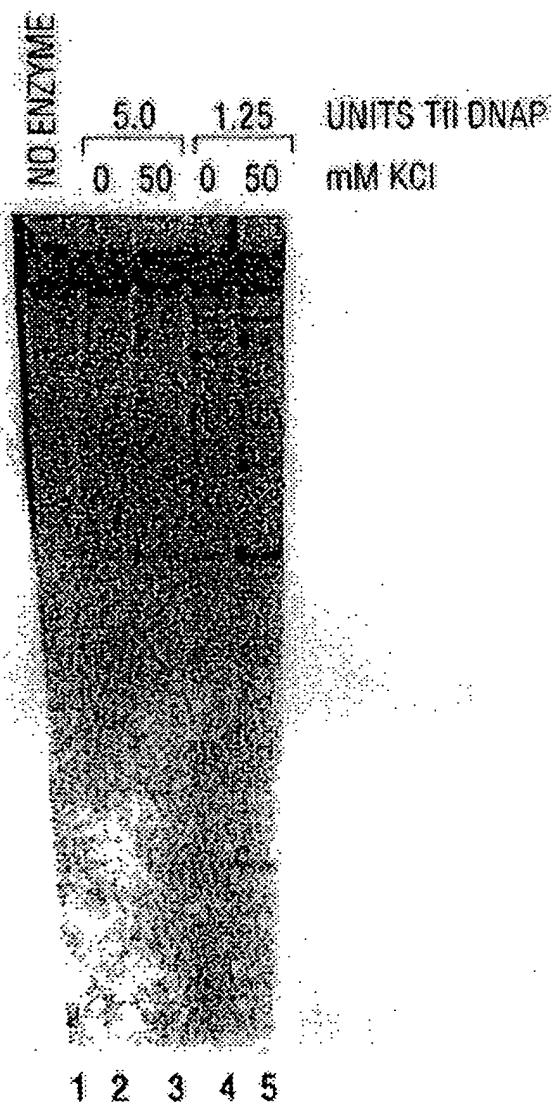


FIG. 67

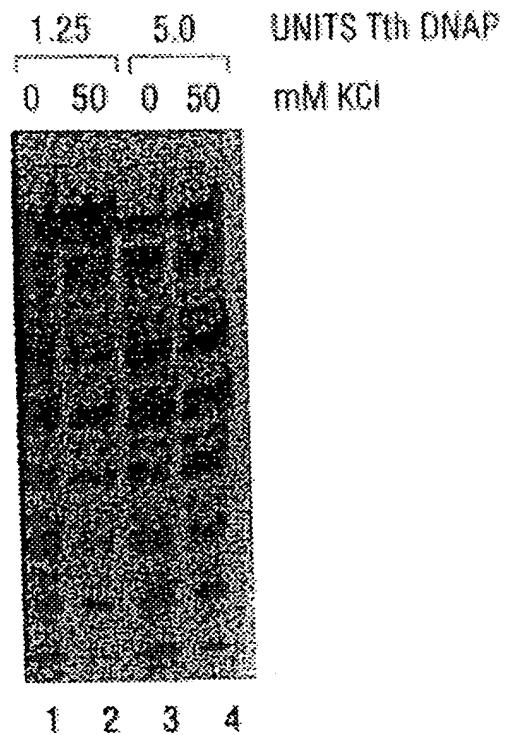


FIG. 68

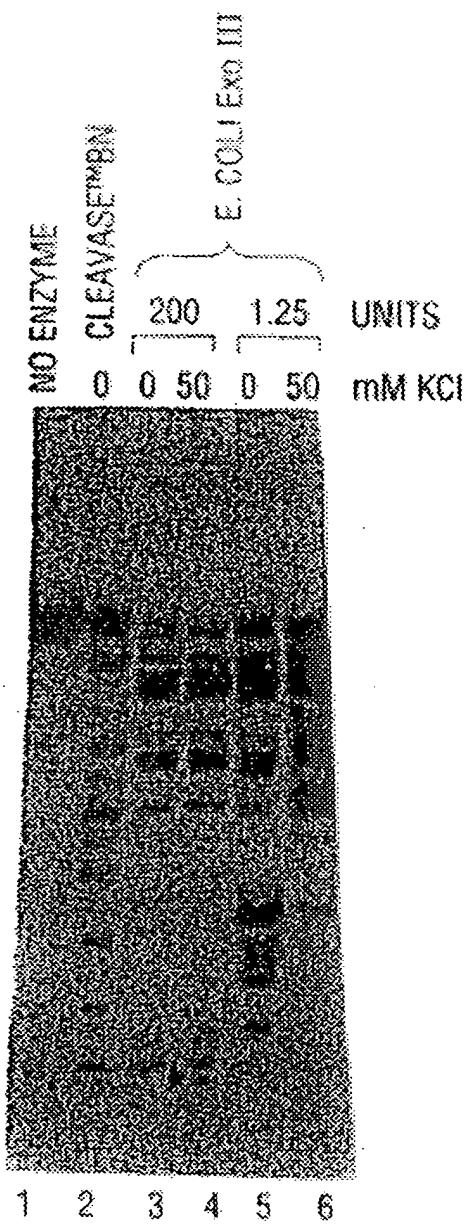


FIG. 69

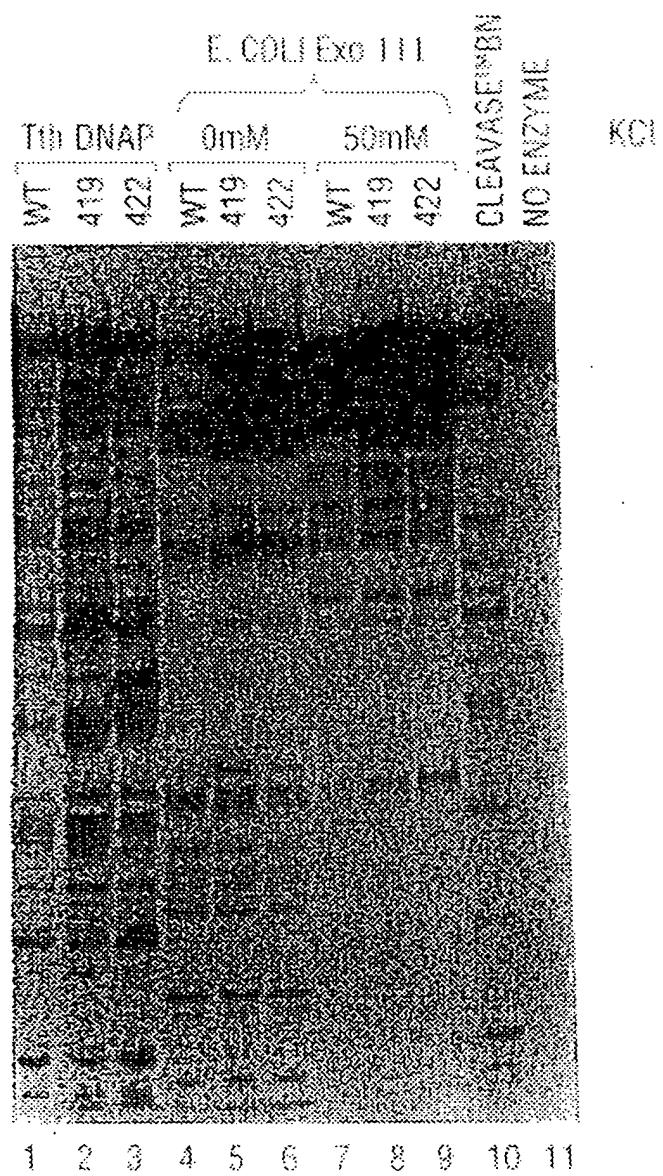
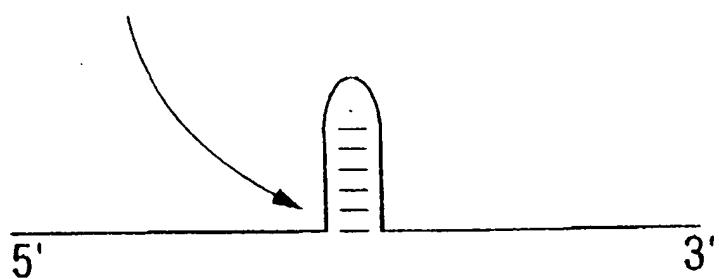


FIG. 70

5' CLEAVAGE SITE



3' CLEAVAGE SITE

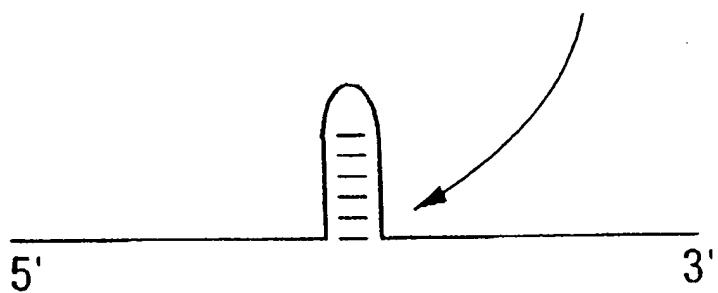


FIG. 71

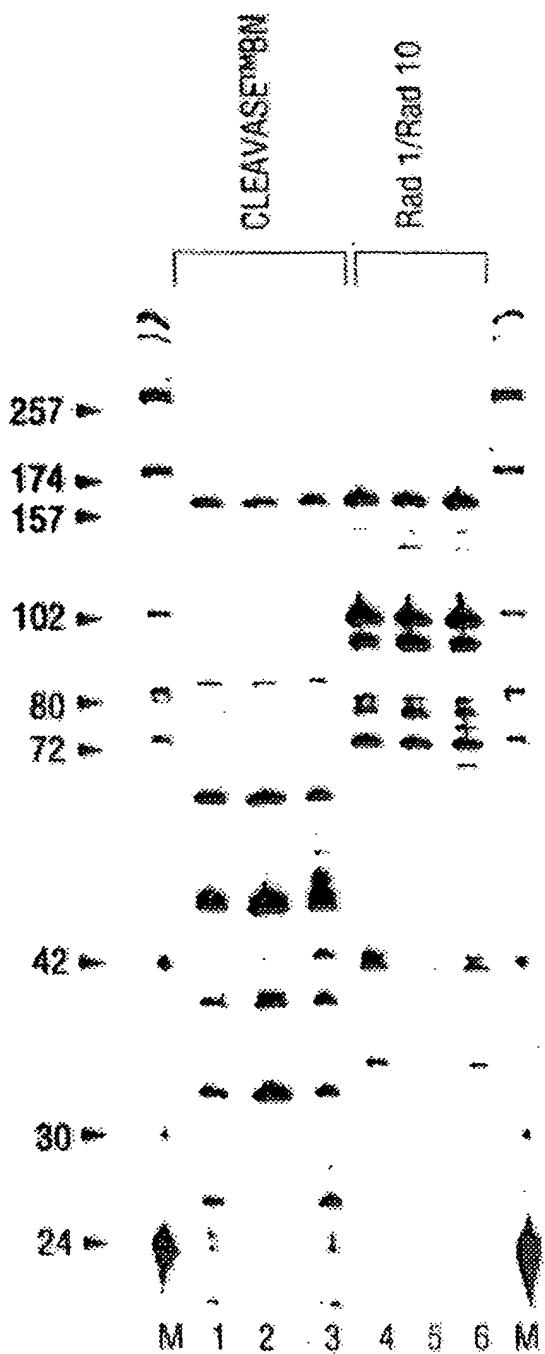


FIG. 72

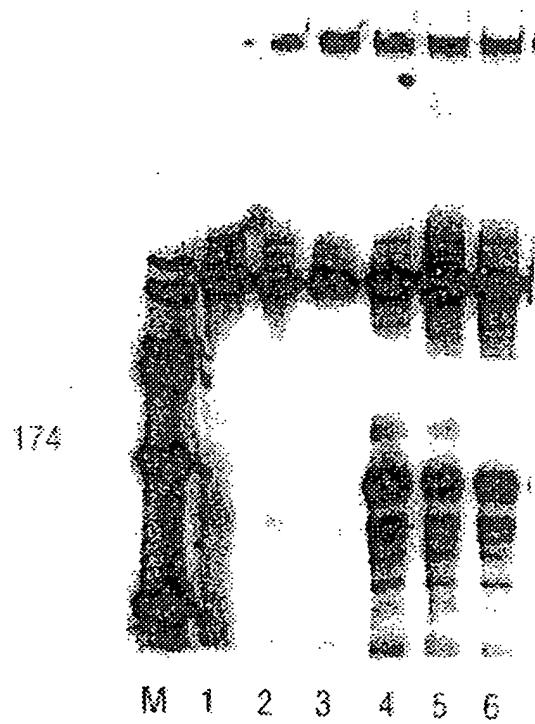


FIG. 73

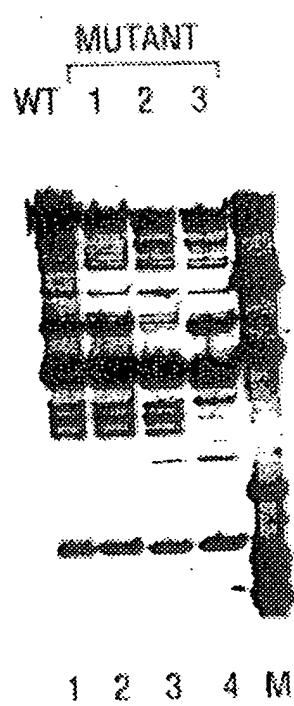


FIG. 74A

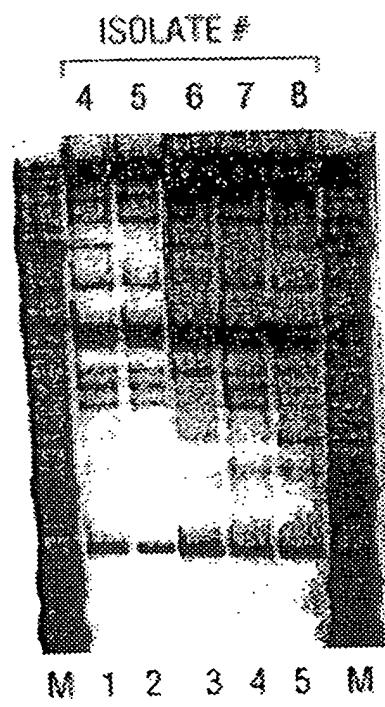


FIG. 74B

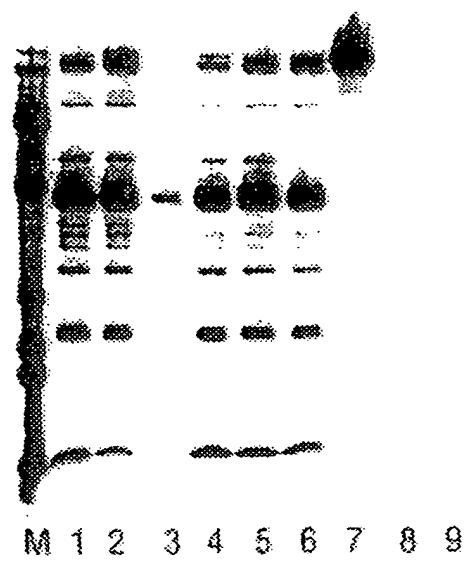


FIG. 75

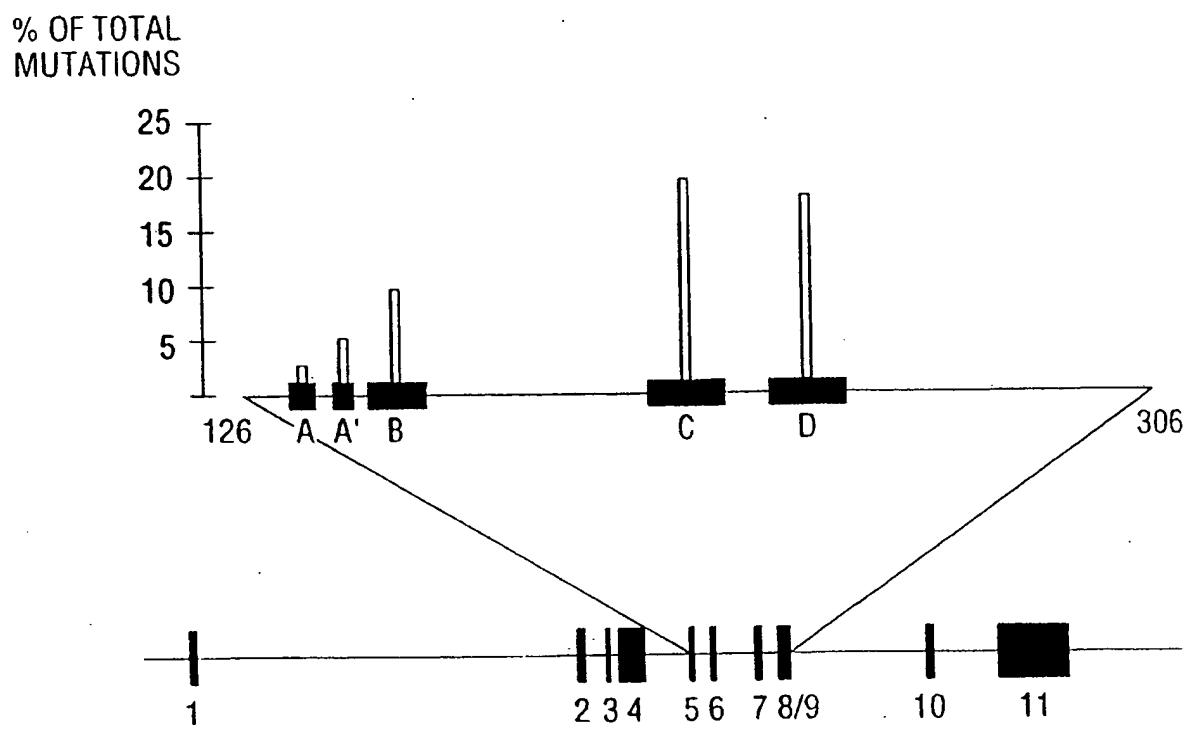


FIG. 76

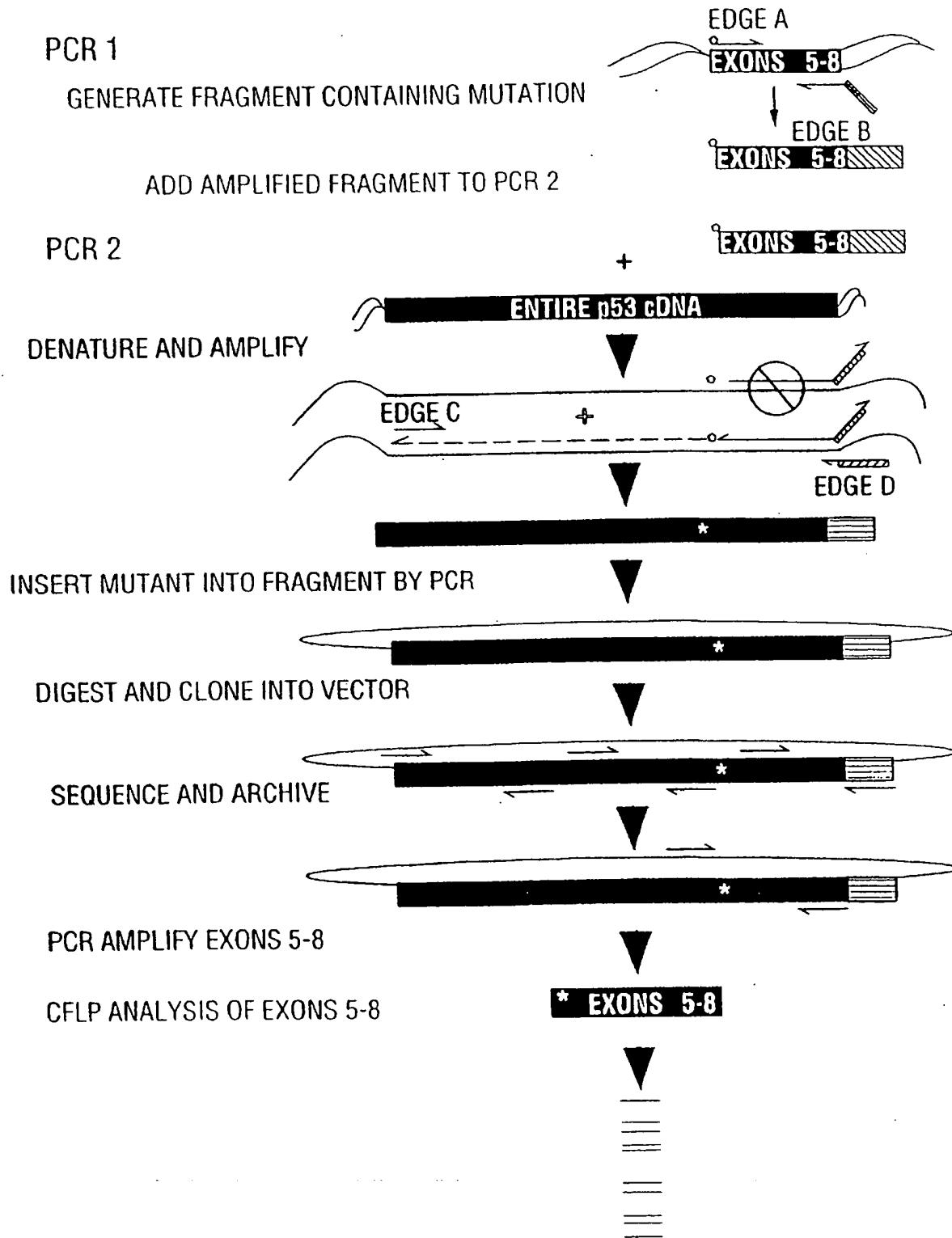


FIG. 77

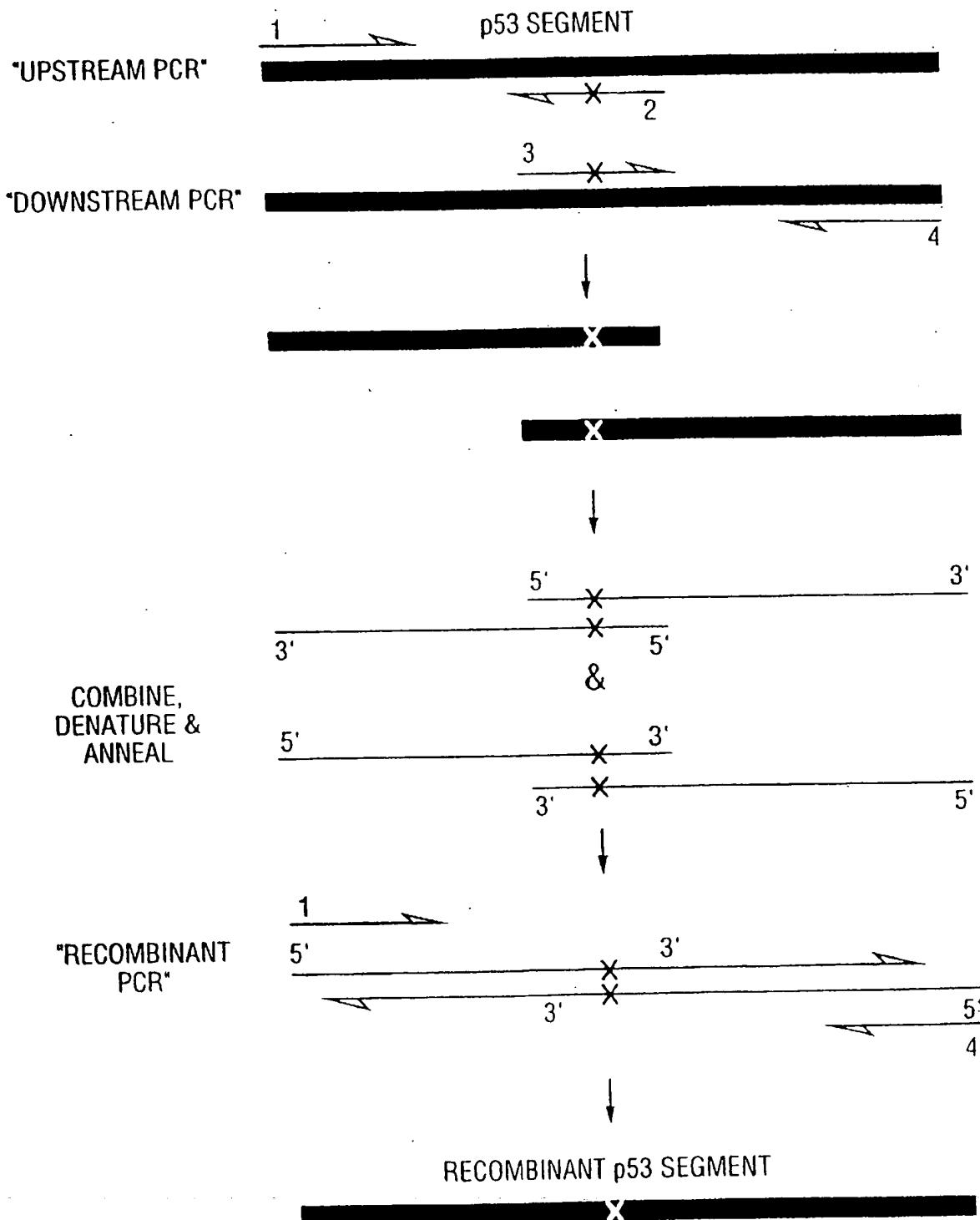


FIG. 78

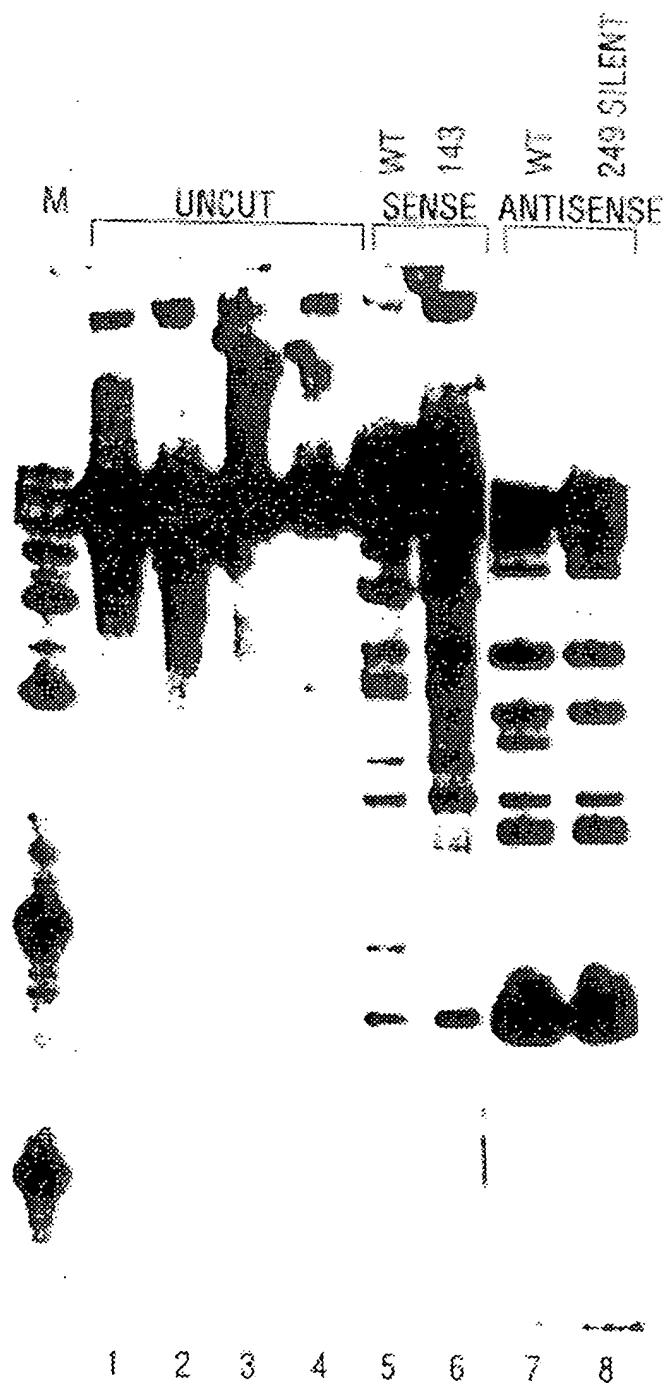


FIG. 79

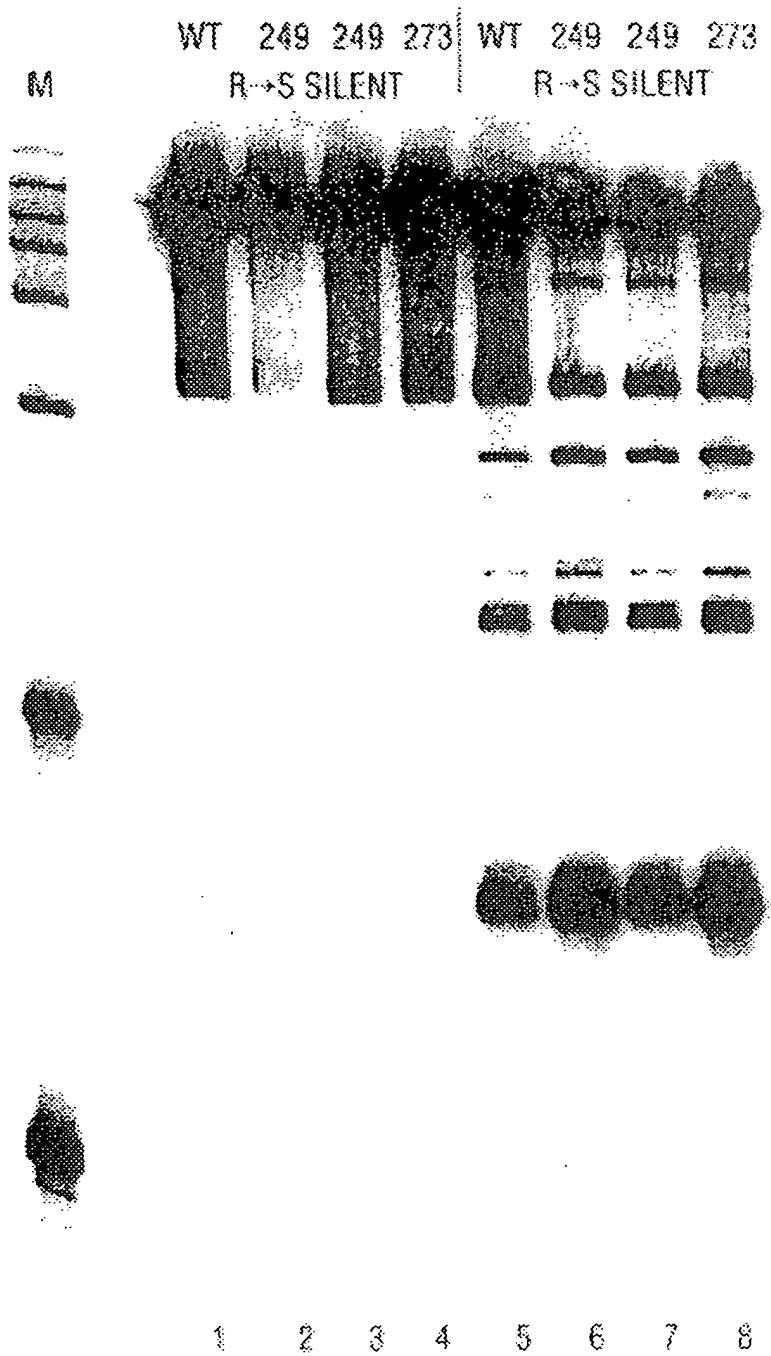


FIG. 80

MIXING PROPORTIONS

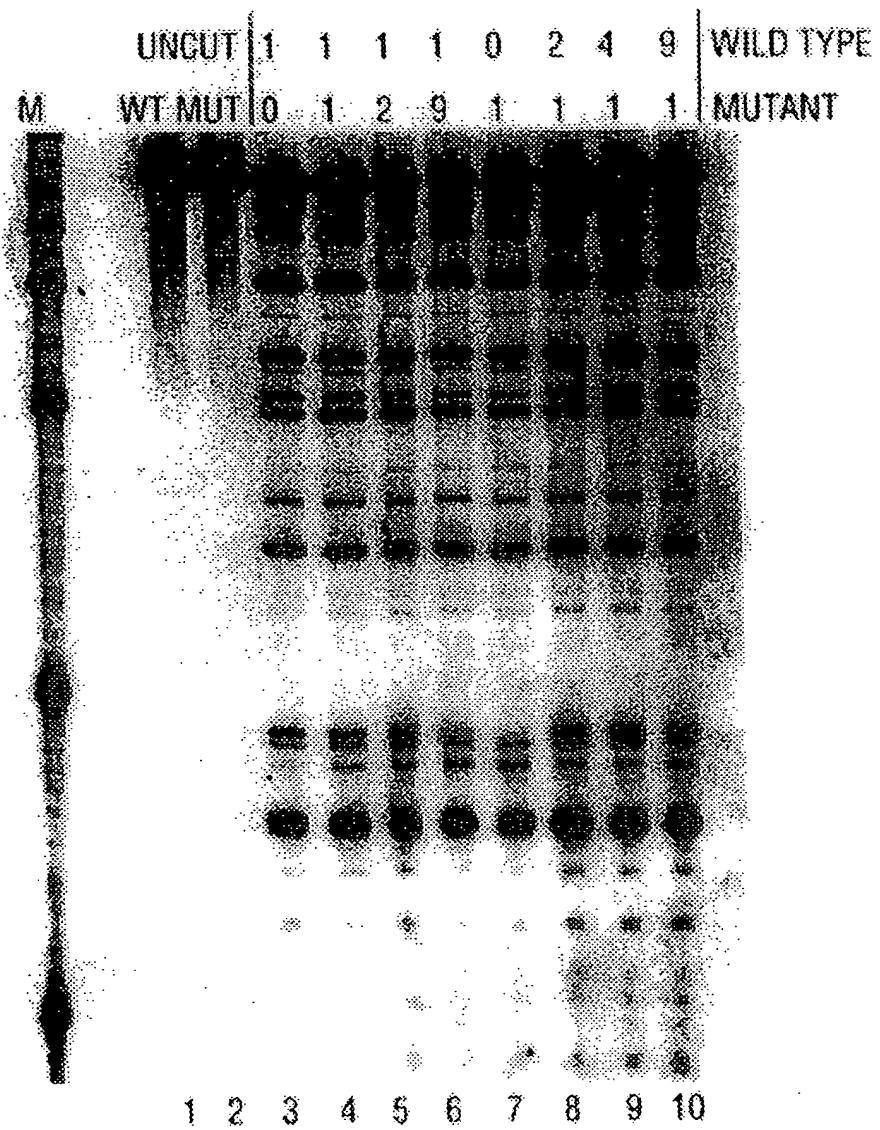


FIG. 81

FIG. 82A

HCV1.1	(SEQ ID NO: 121)	1	CTGTTTCAC	GCAGAAAGCG	TCTGGCCATG	GGGTTAGTAT	GAGTGTCTGT	50
HCV2.1	(SEQ ID NO: 122)		CTGTTTCAC	GCAGAAAGCG	TCTAGCCATG	GGGTTAGTAT	GAGTGTCTGT	
HCV3.1	(SEQ ID NO: 123)		CTGTTTCAC	GCAGAAAGCG	TCTAGCCATG	GGGTTAGTAT	GAGTGTCTGT	
HCV4.1	(SEQ ID NO: 124)		CTGTTTCAC	GCAGAAAGCG	TCTAGCCATG	GGGTTAGTAT	GAGTGTCTGT	
HCV4.2	(SEQ ID NO: 124)		CTGTTTCAC	GCAGAAAGCG	TCTAGCCATG	GGGTTAGTAT	GAGTGTCTGT	
HCV6.1	(SEQ ID NO: 125)		CTGTTTCAC	GCAGAAAGCG	TCTAGCCATG	GGGTTAGTAT	GAGTGTCTGT	
HCV7.1	(SEQ ID NO: 126)		CTGTTTCAC	GCAGAAAGCG	CCTAGCCATG	GGGTTAGTAC	GAGTGTCTGT	
HCV1.1		51	CAGCCTCCAG	GACCCCCCT	CCC GGAGAG	CCATAGTGGT	CTGGGGAAAC	100
HCV2.1			CAGCCTCCAG	GACCCCCCT	CCC GGAGAG	CCATAGTGGT	CTGGGGAAAC	
HCV3.1			CAGCCTCCAG	GTCCCCCT	CCC GGAGAG	CCATAGTGGT	CTGGGGAAAC	
HCV4.1			CAGCCTCCAG	GACCCCCCT	CCC GGAGAG	CCATAGTGGT	CTGGGGAAAC	
HCV4.2			CAGCCTCCAG	GCCCCCT	CCC GGAGAG	CCATAGTGGT	CTGGGGAAAC	
HCV6.1			CAGCCTCCAG	GACCCCCCT	CCC GGAGAG	CCATAGTGGT	CTGGGGAAAC	
HCV7.1			CAGCCTCCAG	GTCCCCCT	CCC GGAGAG	CCATAGTGGT	CTGGGGAAAC	
HCV1.1		101	GGTGAGTACA	CGGAATTGC	CAGGACGACC	GGGTCCTTTC	TTGGAT-AAA	150
HCV2.1			GGTGAGTACA	CGGAATTGC	CAGGACGACC	GGGTCCTTTC	TTGGAT-CAA	
HCV3.1			GGTGAGTACA	CGGAATTGC	CAGGACGACC	GGGTCCTTTC	TTGGAT-CAA	
HCV4.1			GGTGAGTACA	CGGAATTGC	CAGGACGACC	GGGTCCTTTC	<u>GTGGATGIAA</u>	
HCV4.2			GGTGAGTACA	CGGAATTGC	CAGGACGACC	GGGTCCTTTC	TTGGAT-AAA	
HCV6.1			GGTGAGTACA	CGGAATTGC	CAGGACGACC	GGGTCCTTTC	TTGGAT-CAA	
HCV7.1			GGTGAGTACA	CGGAATTGC	<u>TGGGTGACC</u>	GGGTCCTTTC	TTGGAT-CAA	

HCV1 . 1	151	CCC GCT CAAT	GC CT GG AG AT	TT GG CC GT GC	CCC CG CA AG A	CT GCT AG CCC	200
HCV2 . 1		CCC GCT CAAT	GC CT GG AG AT	TT GG CC GT GC	CCC CG CA AG A	CT GCT AG CCC	
HCV3 . 1		CCC GCT CAAT	GC CT GG AG AT	TT GG CC GT GC	CCC CG <u>G</u> AG A	CT GCT AG CCC	
HCV4 . 2		CCC GCT CAAT	GC CT GG AG AT	TT GG CC GT GC	CCC CG CA AG A	CT GCT AG CCC	
HCV6 . 1		CCC ACT CIAT	GC C <u>GG</u> CAT	TT GG CC GT GC	CCC CG CA AG A	CT GCT AG CCC	
HCV7 . 1		CCC GCT CAAT	AC CC <u>GA</u> AT	TT GG CC GT GC	CCC CG <u>G</u> AG A	TC ACT AG CCC	
HCV1 . 1	201	AG TAG T GT TG	GG T CG G AAA	GG C CT TT GT GG	TACT G C CT GA	TAG GGT G <u>C</u> CT	250
HCV2 . 1		AG TAG T GT TG	GG T CG G AAA	GG C CT TT GT GG	TACT G C CT GA	TAG GGT G C TT	
HCV3 . 1		AG TAG T GT TG	GG T CG G AAA	GG C CT TT GT GG	TACT G C CT GA	TAG GGT G C TT	
HCV4 . 2		AG TAG T GT TG	GG T CG G AAA	GG C CT TT GT GG	TACT G C CT GA	TAG GGT G C TT	
HCV6 . 1		AG TAG C GT TG	GG T I G C G AAA	GG C CT TT GT GG	TACT G C CT GA	TAG GGT G C TT	
HCV7 . 1		AG TAG T GT TG	GG T CG G AAA	GG C CT TT GT GG	TACT G C CT GA	TAG GGT G C TT	
HCV1 . 1	251	GG GAG T G CCC	CG GAG GGT CT	CG T AG ACC GT	GC	282	
HCV2 . 1		GG GAG T G CCC	CG GAG GGT CT	CG T AG ACC GT	GC		
HCV3 . 1		GG GAG T G CCC	CG GAG GGT CT	CG T AG ACC GT	GC		
HCV4 . 2		GG GAG T A CCC	CG GAG GGT CT	CG T AG ACC GT	GC		
HCV6 . 1		GG GAG T G CCC	CG GAG GGT CT	CG T AG ACC GT	GC		
HCV7 . 1		GG GAG T G CCC	CG GAG GGT CT	CG T AG ACC GT	GC		

FIG. 82B

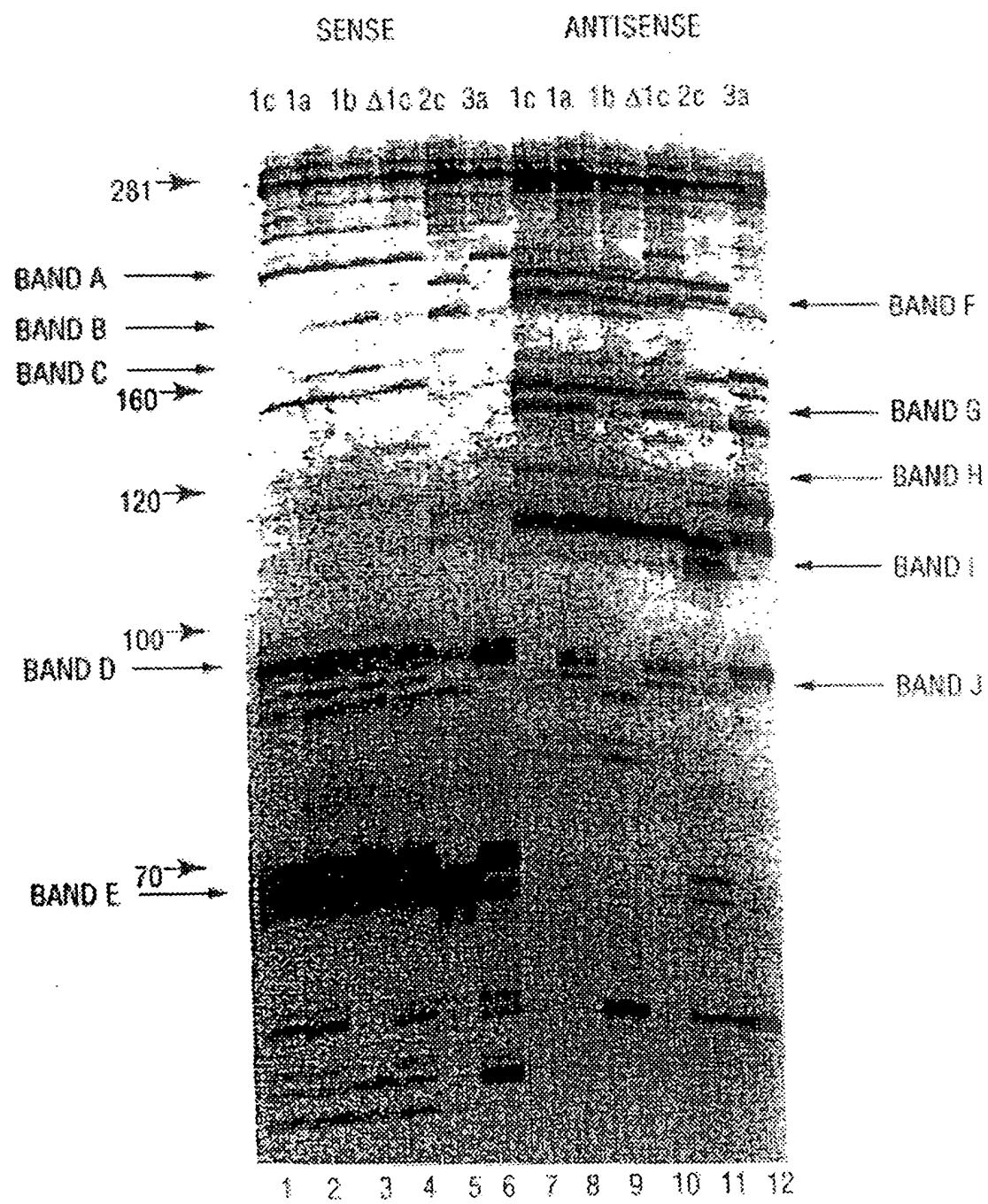


FIG. 83

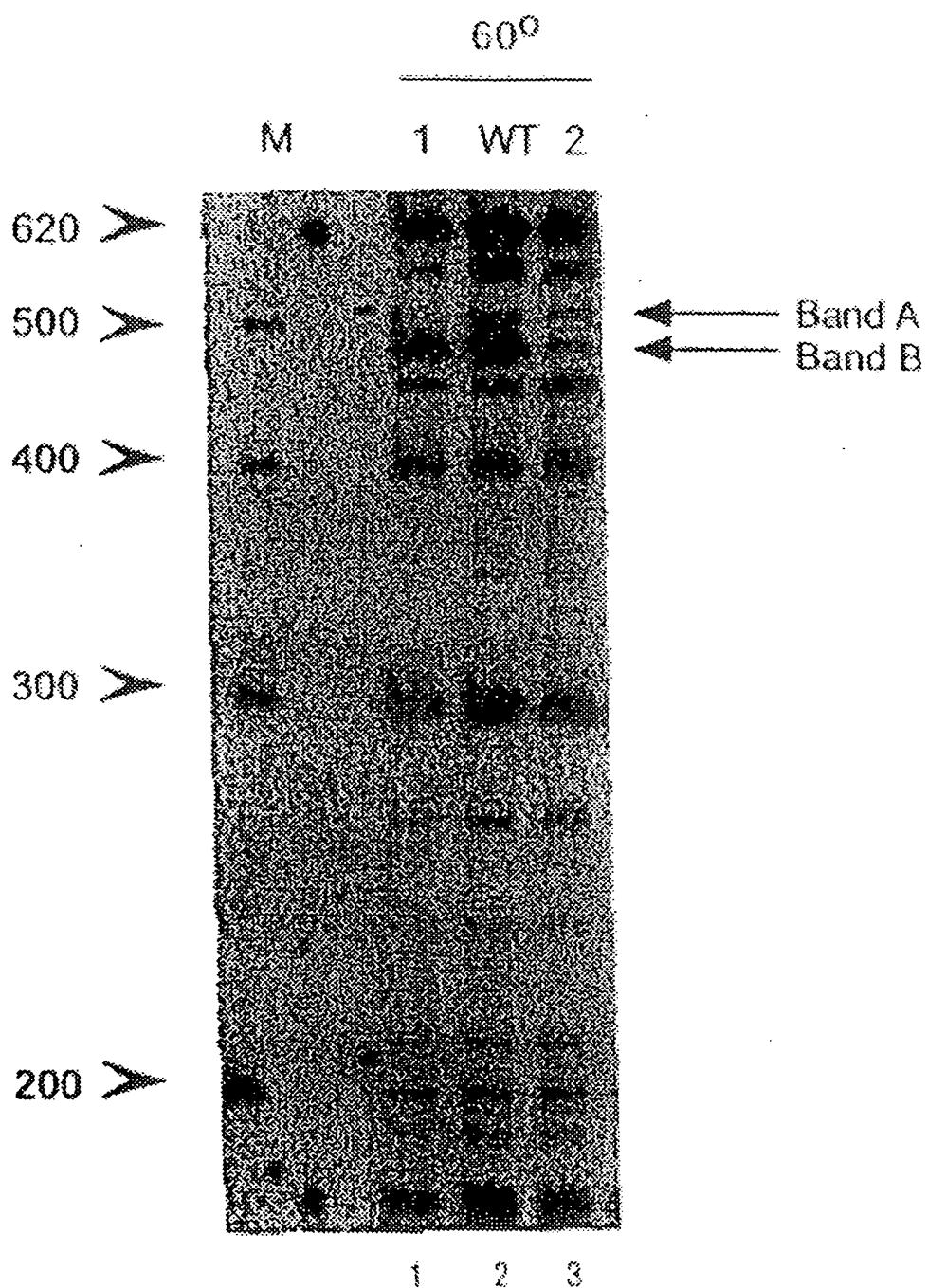


FIG. 84

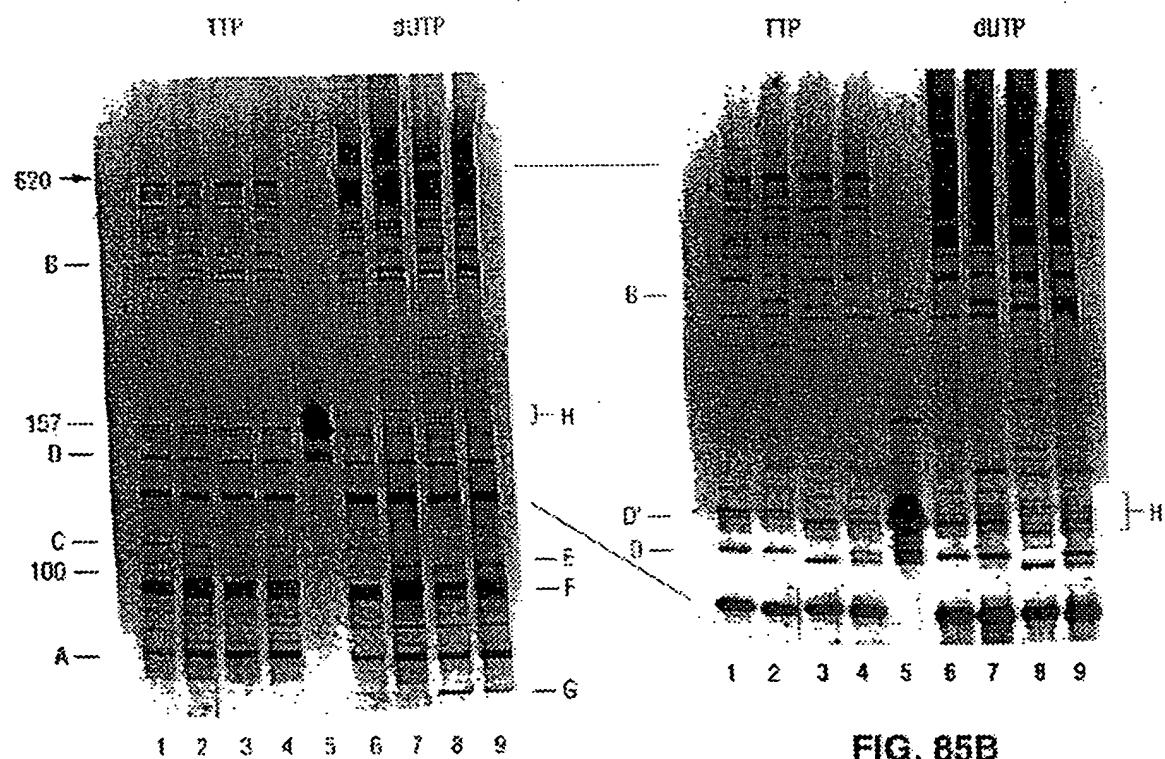


FIG. 85A

FIG. 85B

SENSE STRAND

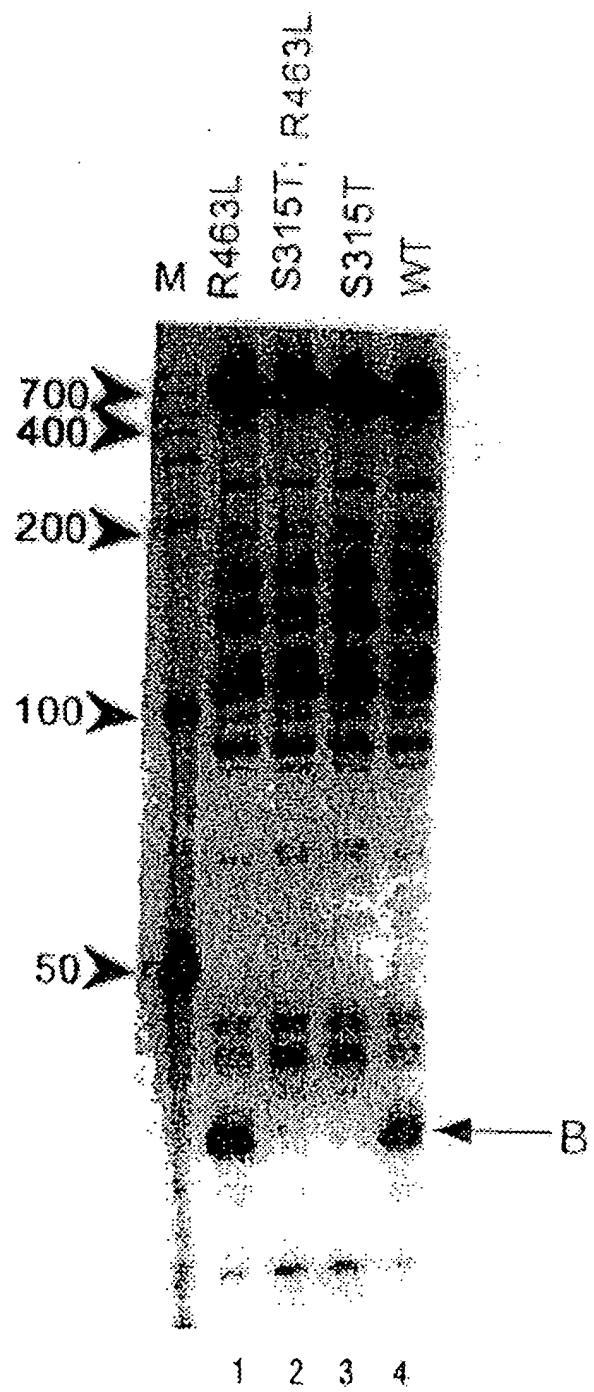


FIG. 86

ANTISENSE STRAND

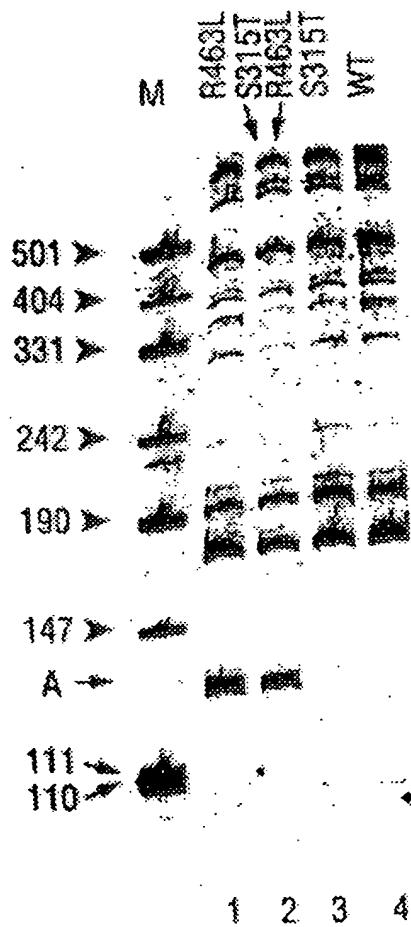


FIG. 87

10	AGA	GTTTGATCCT	<u>GGCTCAG</u>	GAACGCTGGC	GGCAGGCCCTA	ACACATGCAA	1638
	AAATTGAAGA	<u>GTTTGATCAT</u>	<u>GGCTCAGATT</u>	CCGTGGACTAA	CCGTCCGGAT	TGTGTACGTT	
	TTTAACCTCT	CAAACTAGTA	CCGAGTCTAA				
70							
80							
90							
10	GTGGAACCGGT	AACAGGAAGA	AGCTTGCTTC	TTTGCTGACG	AGT <u>GGGGAC</u>	<u>GGGTGAGTAA</u>	ER10
	CAGCTTGCCA	TTGTCCTCT	TCGAACGAAAG	AAACGACTGC	TCACCCGCTG	CCCACACTCATT	
130							
140	TGTCTGGAA	ACTGCCCTGAT	<u>GGAGGGGGAT</u>	AACTACTGGA	AACGGTAGCT	AATAACCGCAT	
	ACAGACCCTT	TGACGGACTA	CCTCCCCCTA	TTGATGACCT	TTGCCATCGA	TTATGGCTA	
190							
200	AACGTCGCAA	GACCAAAAGAG	GGGGACCTTC	GGGCCCTTTG	CCATCGGATG	TGCCCAAGATG	180
	TTGCAAGCGTT	CTGGTTTCTC	CCCCCTGGAAAG	CCCGGAAAC	GTAGCCCTAC	ACGGGTCTAC	
250							
260	GGATTAGCTA	GTAGGGGG	TAACGGCTCA	CCTAGGGGAC	GATCCCTAGC	TGGTCTGAGA	240
	CCTAATCCGAT	CATCCACCCC	ATTGCCGAGT	GGATCCGCTG	CTAGGGATCG	ACCAGACTCT	
310							
320	GGATGACCAAG	CCACACCTGGA	ACTGAGACAC	GGTCCAGACT	CCTAGGGGAG	GCAGGAGTGG	360
	CCTACTGGTC	GGTGTGACCT	TGACTCTGTC	CCAGGTCTGA	GGATGCCCTC	<u>GGTCGTCACC</u>	
						TGA GGATGCCCTC	GGTCGTC
							1659

FIG. 88A

370	380	390	400	410	420
GGAAATATTGC	ACAATGGCG	CAAGCCTGAT	GCAGCCATGC	CGCGTGTATG	AAGAAGGCC
CCTTATAACG	TGTTACCCGC	GTTCGGACTA	CGTCGGTACG	GGCACATAC	TTCTTCCGGA
430	440	450	460	470	480
TCGGGTTGTA	AAGTACTTTC	AGCGGGGAGG	AAGGGAGTAA	AGTTAATACC	TTTGCTCATT
AGCCCACAT	TTCATGAAAG	TGCCCCCTCC	TTCCCTCATT	TCATTATTGG	AAACGAGTAA
490	500	510	520	530	540
GACGTTACCC	GCAGAAGAAG	CACCGGCTAA	CTCCGTGCCA	GCAGCCGGGG	TAATACGGAG
CTGCAATGGG	CGTCTTCTTC	GTGGCCGATT	GAGGCACGGT	CGTCGGGCC	ATTATGCCCTC
550	560	570	580	590	600
GGTGCAAAGCG	TTAACATGGAA	TTACTGGCG	AAAAGGCCAC	GCAGGGGGTT	TGTTAAGTCA
CCACGGTTCGC	AATTAGCCTT	ATGACCCGG	ATTTGGGTG	CGTCCCCAA	ACAATTCACT
610	620	630	640	650	660
GATGTGAAAT	CCCCGGGCTC	AACCTGGGAA	CTGGCATCTGA	TACTGGCAAG	CTTGAGTCTC
CTACACTTTA	GGGGCCGAG	TTGGACCCCTT	GACGTAGACT	ATGACCCGTT	GAACTCAGAG
670	680	690	700	710	720
GTAGAGGGGG	GTAGAATTCC	AGGTGTAGCG	GTGAAATGCC	TAGAGATCTC	GAGGAATAACC
CATCTCCCCC	CATCTTAAGG	TCCACATGCC	CACTTTACGC	ATCTCTAGAC	CTCCTTATGG
730	740	750	760	770	780
GGTGGCGAAG	GGGGCCCCCT	GGACGAAAGAC	TGACGGCTCAG	GTGCGAAAGC	GTGGGGAGCA
CCACGGCTTC	GGGGGGGA	CCTGCTTCTG	ACTGCGAGTC	CACGCTTTCG	CACCCCTCGT

FIG. 88B

AACAGGATTA TTGTCCATA	790	800	810	820	830	840
		GATACCCCTGG CTATGGACC	TAGTCCACGCC ATCAGGTGGC	CGTAAACGAT GCATTGGCTA	GTCGACTTGG CAGCTGAACC	AGGTTGTGCC TCCAACACGG
CTTGGGGGT	850	860	870	880	890	900
GAACCTCCGCA		GCTTCCGGA CGAACGGCCT	GCTAACGGGT CGATTGGCA	TAAGTCGACC ATTCAAGCTGG	GCCTGGGGAG CGGACCCCTC	TACGGCCGGCA ATGCCGGCGT
AGGTTAAC TCCAATTGG	910	920	930	940	950	960
		TCAAATGAAAT AGTTTACTTA	TGACGGGGC ACTGGCCCCG	CCGCACAAAGC GGGTGTTTG	GGTGGAGCAT CCACCTCTGTA	GTGGTTTAAT CACCAAATTA
TCGATGCAAC AGCTACGTTG	970	980	990	1000	1010	1020
		GGGAAGAAC CGTTCTTGG	TTACCTGGTC AATGGACCAAG	TTGACATCCA AACTGTAGGT	CGGAAGTTT GCCCTTCAAA	CAGAGATGAG GTCTCTACTC
AATGTGCTT TTACACGGAA	1030	1040	1050	1060	1070	1080
		GGGAACCGT GCCCTGGCA	GAGACAGGGT CTCTGTCCAC	CTGGCATGGCT GACGTACCGA	GTCGTCAGCT CAGCAGTCCGA	CGTGTGTTGA GCACAAACACT
	1090	1100	1110	1120	1130	1140
		GC GC	AACGAGGGCA ACCC			
AATGTTGGT TTACAACCA		TAAGTCCGGC ATTCAAGGGC	AACGAGGGCA TTGCTCGGGT	ACCCCTTATCC TGGAAATTAGG	TTTGTGCCA AAACAACGGT	GGGGTCCGGC CGCCAGGGCG
	1150	1160	1170	1180	1190	1200
CGGGAACCTCA CCCCCTTACCT						
		CACTGATAA GTCACTATT	ACTGGAGGAA TGAACTCTT	GGTGGGGAG CCACCCCCCTAC	ACGTCAAGTC ACGTCAAGTC	SB-3 SB-4

88C
EIG

1210	1220	1230	1240	1250	1260	
ATCATGGCCC	TTA					SB-3
ATCATGGCCC	TTACGA					SB-4
<u>ATCATGGCCC</u>	<u>TTACGACCAG</u>	<u>GGCTACACAC</u>	<u>GTGCTACATA</u>	<u>GGCCGATACA</u>	<u>AAGAGAACCG</u>	
TAGTACCGGG	AATGCTGGTC	CCGATGTGT	CACGATGTTA	CCGGTATGT	TTCTCTTGGC	
1270	1280	1290	1300	1310	1320	
ACCTCGCGAG	AGCAAGCGGA	CCTCATAAAG	TGCCGTCGTAG	TCCGGATTGG	AGTCTGCAAC	
TGGAGCGCTC	TGGTTCGGCT	GGAGTATTTC	ACGCAGCATE	AGGCCTAACCC	TCAGACCGTTG	
1330	1340	1350	1360	1370	1380	
TCGACTCCAT	GAAGTCCGAA	TCGCTAGTAA	TGGTGGATCA	GAATGCCACG	GTGAATAAGT	
AGCTGAGGTA	CTTCAGCCCTT	AGCGATCATT	ACGACCTAGT	CTTACCGTGC	<u>CACCTTATGCA</u>	
				GC	CACTTATGCA	1743
1390	1400	1410	1420	1430	1440	
TCCCGGGCT	TGTACACACC	GCCCCGTACACA	CCATGGGAGT	GGGTTGCCAA	AGAAGTAGGT	
<u>AGGGCCCCGA</u>	<u>ACATGTTGG</u>	<u>CGGGCAGTGT</u>	<u>GGTACCCCTCA</u>	<u>CCCAACGTTT</u>	<u>TCTTCATCCA</u>	
						1743
1450	1460	1470	1480	1490	1500	
AGCTTAACCT	TGGGAGGGC	GCTTACCACT	TTGTGATTCA	TGACTGGGT	GAAGTCCGTA	
TCGAATTGGA	AGCCCCTCCG	CGAATGGTGA	AACACTAAGT	ACTGACCCCA	CTTCAGCATT	
1510	1520	1530	1540	1550		
CAAGGTAACC	GTAGGGGAAC	CTGGGGTGG	ATCACCTCT	TA.....		
GTTCCATTGG	CATCCCCCTTG	GACGCCAACCC	TAGTGGAGGA	AT.....		

FIG. 88D

1638 (SEQ_ID NO:151)	AGAGTTTGAATCCTGGCTCAG	
E.colirrSE (SEQ_ID NO:158) 0	AAATTGAAGAGTTGATCATGGCTCAGATTGAACGGCTAACACACATGCA	
Cam.jejuns (SEQ_ID NO:159) 0	-TTTTTATGGAGAGTTGATCTGGCTCAGGTGAACGGCTGGCTTAATACATGCA	
Stp.aureus (SEQ_ID NO:160) 0	.TTTTATGGAGAGTTGATCTGGCTCAGGTGAACGGCTGGCTTAATACATGCA	
		GGGGGACGGG
ER10 (SEQ_ID NO:152)	TGAGTAA	
E.colirrSE	114 TGAGTAATGTCCTGGGA-AACTGCCATGGAGGGATAACTACTGGAAACGGTAGCTAATA	
Cam.jejuns	114 TGAGTAAGGTATACTTTAACACAGTTGGAAACGACTGGCTTAATA	
Stp.aureus	113 TGAGTAACACGTGATAACCTACCTATAAGACTGGATAACTTGGAAACCGGAGCTAATA	
E.colirrSE	175 CCGCATAAC-GTGCAGAAC-CAAGAGGGGACCTTCG=GCCCTCTTG	
Cam.jejuns	176 CTCTATACTCCTGCTTAACACAAGTTGAGTAGG-GAAAG-TTTTT-----CG	
Stp.aureus	175 CGGATAATTTGAACGGCATGGTCAAAGTGAAGACGGT---CTT---GCTGTCAC	
E.colirrSE	221 CCATGGATGTGCCAGATGGATTAGCTAGTAGGTGGGTAACGGCTACGGGAGCA	
Cam.jejuns	221 GTGTAGGATGAGACTATATAGTATGGCTTAAGGTAAAGCTATGAG	
Stp.aureus	229 CTTATAGATGGATCCGGCTGATTAGCTAGTTGGTAAGGTAAAGGGCTTACCAAGGCAACGA	
E.colirrSE	283 TCCCTAGCTGGCTTGAGGATGACCACTGGAACTGGACACGGCTCAGACTCCCTA	
Cam.jejuns	283 CCTTAACCTGGCTTGAGGATGATCAGTCACACTGGAACTGGACACGGCTCAGACTCCCTA	
Stp.aureus	291 TACGTAGCCGACCTGAGGGTGTGACACTGGAACTGGACACGGCTCAGACTCCCTA	
1659 (COMPL)	ACTCCCTA	

FIG. 89A

E. coli rrSE	CGGGAGGCAGCAGTGGGGAAATATTGCAACAAATGGGCCAAGGCTGATGCGCCATGCCCGCTG	345
Cam. jejuns	CGGGAGGCAGCAGTGGGGAAATATTGCAACAAATGGGCCAAGGCTGATGCGCCATGCCCGCTG	345
Stp. aureus	CGGGAGGCAGCAGTGGGGAAATATTGCAACAAATGGGCCAAGGCTGATGCGCCATGCCCGCTG	353
1659 (COMPL)	CGGGAGGCAGCAGTGGGGAAATATTGCAACAAATGGGCCAAGGCTGATGCGCCATGCCCGCTG	
E. coli rrSE	TATGAAGAAGGCCCTGGGTTAAAGTACTTTCAAGGGGGAGGAA - GGGAGTAAAGTTAAT	407
Cam. jejuns	GAGGATGACACCTTTGGAGCGTAAACTCCTTTCTTAGGAAAG <u>-----</u> ATGTGTAAGTAAAC	407
Stp. aureus	AGTGTGAAGGTCTGGATCGTAAAACTCTGTATTAGGAAAGAACATATGTGTAAGTAAAC	415
E. coli rrSE	ACCTTTGCTCATTTGACGTTACCCGAGAAAGCACCGGCTAACTCCGGTCCCAGGCCGGC	468
Cam. jejuns	C-----TGACGGTACCTAAGGAATAAGCACCGGCTAACTCCGTGCCAGGCCGGC	455
Stp. aureus	=TGTGCACATCTTGACGGTACCTAAGAACGCAACGGCTAACTACGTGCCAGGCCGGC	476

FIG. 89B

<i>E. coli</i> rrSE	530	GTAATAACGGAGGGTCCAAGCGTTAACCGGAAATTACTGGCATTAAAGCCACGGAGGGTT
<i>Cam. jejuni</i> 5	506	GTAATAACGGAGGGTCCAAGCGTTAACCGGAAATTACTGGCATTAAAGCCACGGAGGGATT
<i>Stp. aureus</i>	538	GTAATAACGTAGGTGCCAACGGTTATCCGGAAATTATTGGCGTAAAGCCGTTAGGGGTTT
<i>E. coli</i> rrSE	592	TTAAGTCAGATGTGAAATCCCCGGCTCAACCTGGAAACTGGCATCTGATACTGGCATTGGAGCTT
<i>Cam. jejuni</i> 5	568	ATCAAGTCTTGTGAAATCTAACCTAAACTGGCTTAACCTAAACTGGATACTGATAGTCTA
<i>Stp. aureus</i>	600	TTAAGTCTGATGTGAAAGCCACGGCTAACCGGCTAACCGGAGGGTCAATTGGAAACTGGAAAACCT
<i>E. coli</i> rrSE	654	GAGTCTCGTAGAGGGGGTAGAAATTCCAGGTGTAGCGGTGAAATGCGTAGAGATCTGGAGGA
<i>Cam. jejuni</i> 5	630	GAGTGAGGGAGAGGCAGATGGAAATTGGTGGTAGGGGTAAATTCGGTAACTGGAGATAATGGAGGA
<i>Stp. aureus</i>	662	GAGTGCAGAAGAGAAATGGAAATTCCATGTGTAGCCGTGAAATGGCAGAGATAATGGAGGA
<i>E. coli</i> rrSE	716	ATACCGGTGGCGAAGGGGGCCCTGGACGAAGAAGACTGACCGCTCAGGTGCGAAAGCCGTGGGA
<i>Cam. jejuni</i> 5	692	ATACCCATTGGCAAGGGGATCTGGAAACTCAACTGACCGCTAACGGCTAAAGGGGGATCTGGGT
<i>Stp. aureus</i>	724	ACACCAGTGGCGAACGGGACTTCTGGCTGTAACTGACCGCTGATGTGCGAAAGGGTGGGA
<i>E. coli</i> rrSE	778	GCAAACAGGATTAGATAACCGTACGGATGTCGACTTGGAGGTTGTGCG
<i>Cam. jejuni</i> 5	754	GCAAACAGGATTAGATAACCCCTGGTAGTCAACTAGTGTACCTAAACGATGTGTTGGGGT
<i>Stp. aureus</i>	786	TCAAACAGGATTAGATAACCCCTGGTAGTCCACGGCGTAAACGATGTCAAGTGTGGGG

FIG. 89C

FIG. 89D

SB-3	(SEQ ID NO: 157)	ATGACCGTCAAGTCATC
SB-4	(SEQ ID NO: 154)	ATGACCGTCAAGTCATC
<i>E. coli</i> rrSE	1142	GGGAACCTCAAAGGAGACTGCCAGTGATAAACTGGAGGAAGGTGGGGATGACCTCAAGTCATC
<i>Cam. jejuns</i>	1122	GAGCACTCTAAATAGACTGCCCTCG=TAAGGAGGAGGAAGGTGGGACGCTCAAGTCATC
<i>Stp. aureus</i>	1152	GGGCACTCTAAGTTGACTGCCGGTACAATGGGATGACCTCAAGGTGGGAGGAACCCGGAGGAAACCAAAACCGGAGGAAAGGTGGGATGACCTCAAAATCATC
SB-3		ATGGCCCTTA
SB-4		ATGGCCCTTAGGA
<i>E. coli</i> rrSE	1204	ATGGCCCTTACGGACCAAGGGCTCACACACGTGGCTACAATTGGCATATAGAAATGAGACGCCATTAC
<i>Cam. jejuns</i>	1183	ATGGCCCTTATGCCCAAGGGGACACACGTGGCTACAATTGGCATACAAAGGGAGGAAACC
<i>Stp. aureus</i>	1214	ATGGCCCTTATGGATTGGCTACACACGTGGCTACAATTGGCATACAAAGGTGGCAACTCGACTC
<i>E. coli</i> rrSE	1266	GGGAGGAAAGCCGGAACCTCATAAAGTGGCTGTAGTCCGGATTGGAGTCTGCAACTCGACTC
<i>Cam. jejuns</i>	1245	GGGAGGTTGGAG-CAAACTATAAAATATGTCGGATTGGATTCTGCAACTCGAGAG
<i>Stp. aureus</i>	1276	GGGAGGTCAGGAAATCCCATAAAAGTTGGATTCTCAGTTCGGATTGTAGTCTGCAACTCGACTA
<i>E. coli</i> rrSE	1328	CATGAAGTCGGAATCGCTAGTAATCGTGGATCAGA-ATGCCACGGTGAATACTGGGGC
<i>Cam. jejuns</i>	1306	CATGAAGCCGGAAATCGCTAGTAATCGTGGATCAGGCTACGGTACGGTAAATACGTTCCCCGGT
<i>Stp. aureus</i>	1338	CATGAAGCTGGAAATCGCTAGTAATCGTGGATCAGGCTACGGTACGGTAAATACGTTCCCCGGT
1743 (compl)		

FIG. 89E

<i>E. coli</i> rrSE	1389	CTTGTACACCCGGCGTACACCATGGAGTGGGTTGAAAGTAGGTAGCTTAACCT
<i>Cam. jejuni</i> 5	1368	CTTGTACTCACCCGGCGTACACCATGGAGTTGATTCACTCGAACGGGAATACT--A-A
<i>Stp. aureus</i>	1399	ATTGTACACCCGGCGTACACCATGGAGTTGAAACACCCGAAGGGTGGAGTAACCT
1743 (compl)		CTTGTAC
<i>E. coli</i> rrSE	1451	TGGGGGCTTACCACTTGTGATTCATGACTGGGTGAAGTCGTAAACAAAGGTAAACCG
<i>Cam. jejuni</i> 5	1427	AC---T-AGTTACCGTCCACAGTGGAACTAGGGACTGGGTGAAGTCGTAAACAAAGGTAAACCG
<i>Stp. aureus</i>	1461	TTTAGGAGCTAGCCCCGTGAAGGTGGACAATGATTGGGTGAAGTCGTAAACAAAGGTAGCCG
<i>E. coli</i> rrSE	1512	TAGGGAACCTGGGTTGGATCACCTTTA---
<i>Cam. jejuni</i> 5	1485	TAGGAGAACCTGGGTTGGATCACCTCT---
<i>Stp. aureus</i>	1523	TATCGGAAGGTGGGCTGGATCACCTCTTTCT-

FIG. 89F

1 2 3 4 5 6 7 8

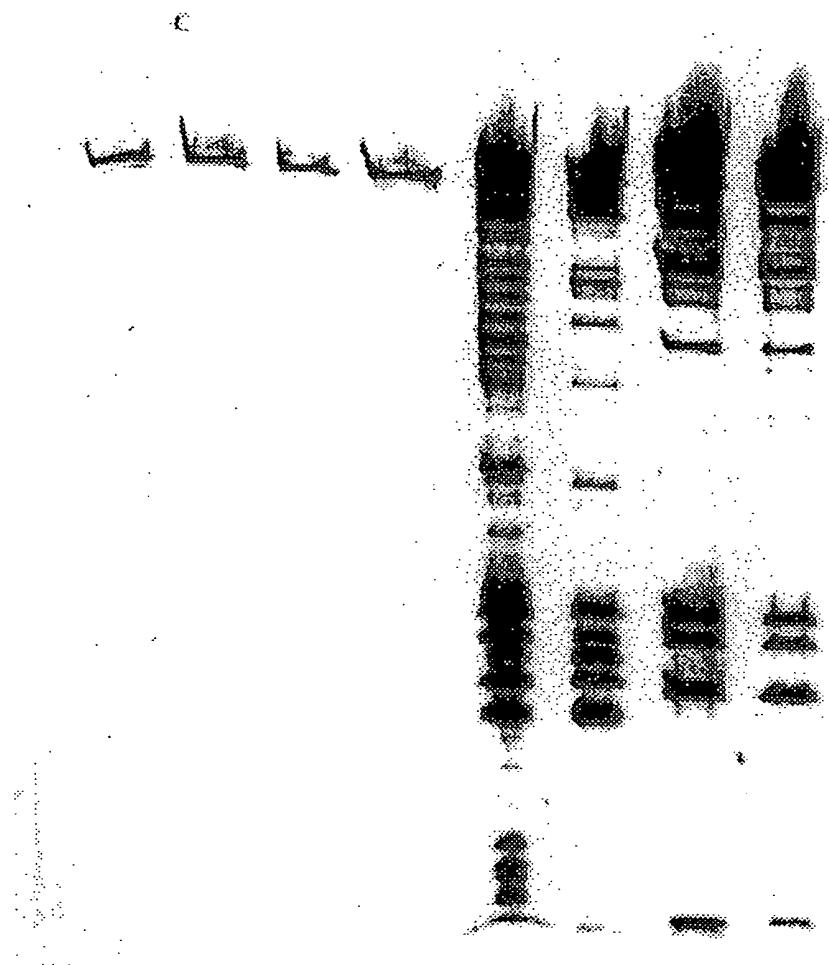


FIG. 90

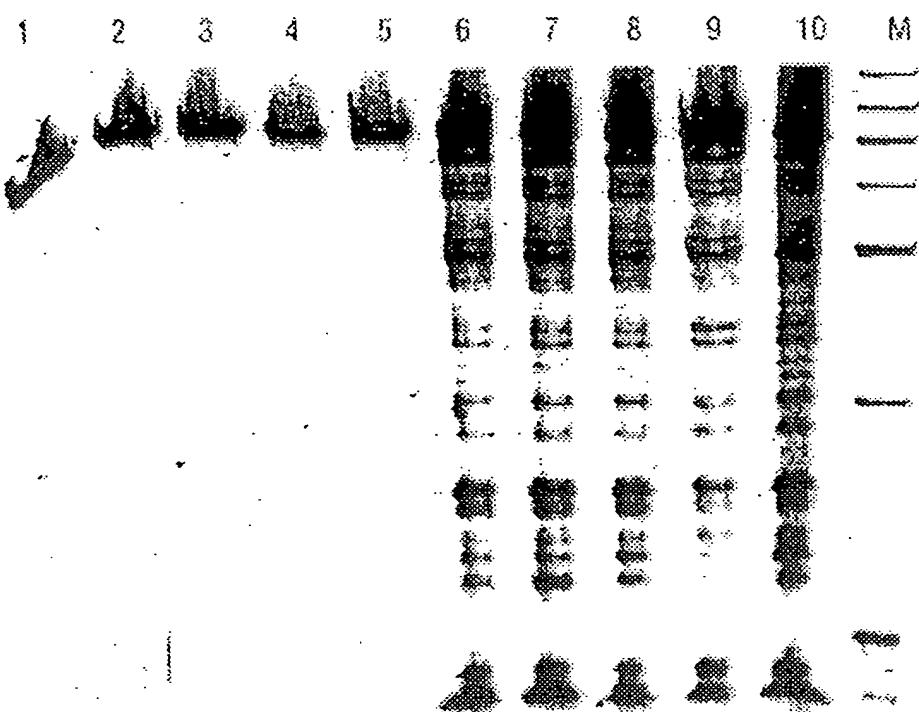


FIG. 91A

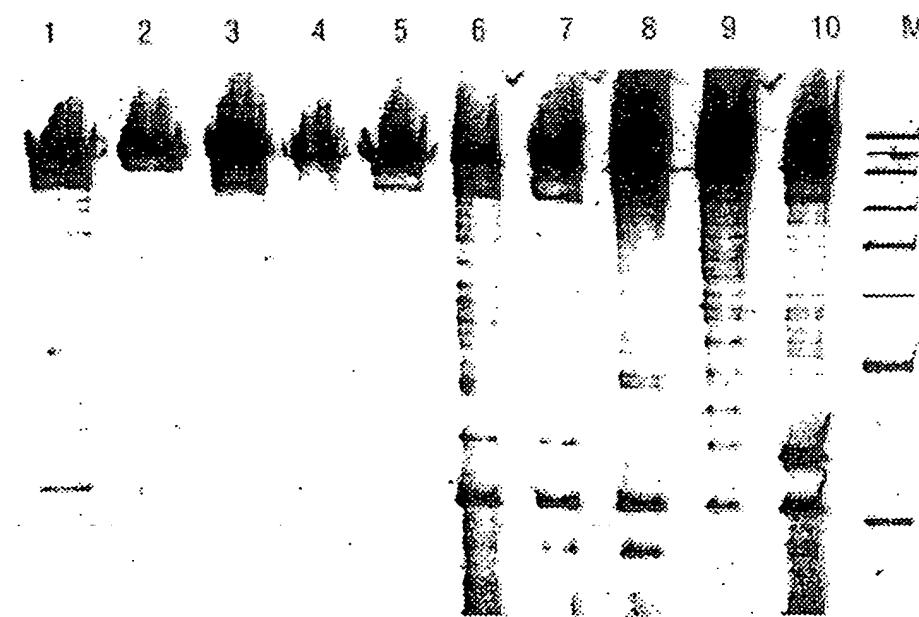


FIG. 91B

1 2 3

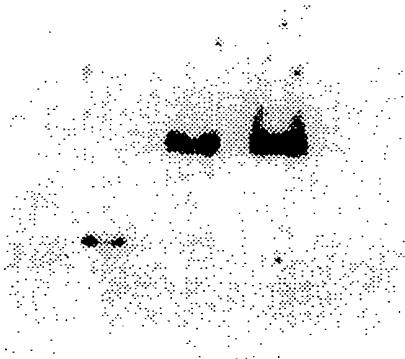
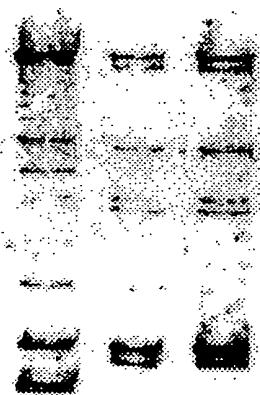


FIG. 92

1 2 3 4 5 6 7 8

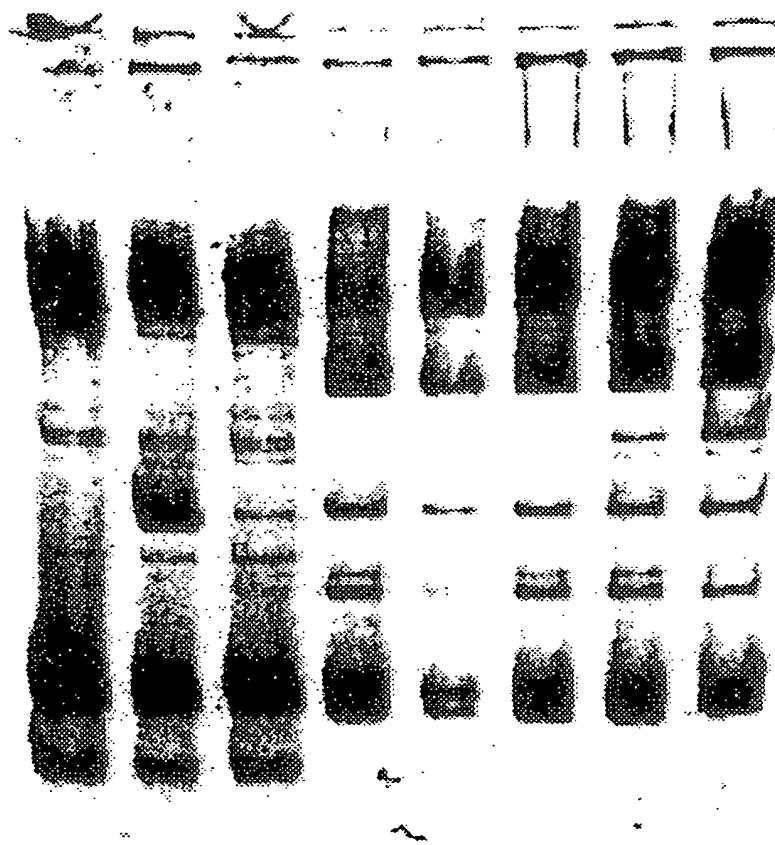


FIG. 93

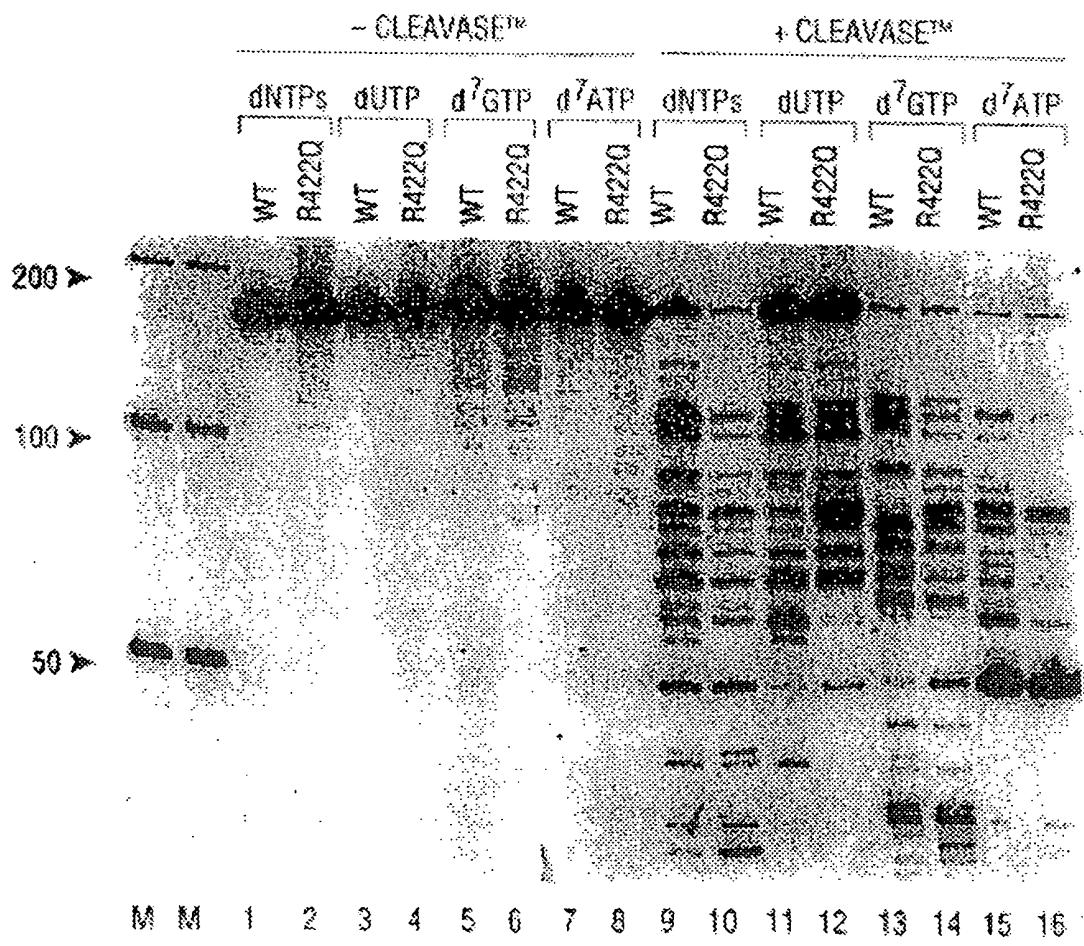


FIG. 94